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P83328 oncor
P18818 prote
Q09261 caeno
Q9br76 homo
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Q9411 vibri
P24620 micrc
Q83879 trepc
P24621 micrc
Q83879 trepc
P35111 homo
Q9zcs8 rick
Q09237 caen
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Q9538 sacc
Q94017 cand
Q94013 sacc
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caenorhabdi
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SEQUENCE ..... SPECIES-Human, and Mouse; SPECIES-Human, and Mouse; MEDLINE-93368957; PubMed-8395683; MEDLINE-93368957; PubMed-8395683;

SEQUENCE FROM N.A.

SPECIES-Mouse: STRAIN-BALB/c; MEDLINE-95241522; PubMed-7724584; Nakamura M., Xavier R.M., Tsunematsu T., "Molecular cloning and characterization nonspecific suppressor factor."; Proc. Natl. Acad. Sci. U.S.A. 92:3463-34

."; 92:3463-3467(1995).

, Tanigawa of a cDNA

encoding

monoclonal

SEQUENCE FROM N.A.

"The carboxyl extension of a ubiquitin-like protein protein S30.";
J. Biol. Chem. 268:17967-17974(1993).

ls

rat ribosomal

SEQUENCE FROM N.A., AND SEQUENCE OF 1-18.
SPECIES=Rat; STRAIN-Sprague-Dawley; TISSUE=Liver;
MEDLINE=93352612; PubMed=8394356;

Olvera J., Wool I.

<u>.</u>

sarcoma virus.";
Oncogene 8:2537-2546(1993).

expressed as an antisense sequence

encodes a ubiquitin-like-S30 fusion protein and is as an antisense sequence in the Finkel-Biskis-Reilly murine

van

Hasselt F.,

Kas

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CDNA

Michiels L., v Merregaert J.;

SPECIES-Mouse; STRAIN-BALB/c; TISSUE-Liver; MEDLINE-95293388; PubMed-7774934; Casteels D., Poirier C., Guenet J.-L., Meri

J.-L., Merregaert J.;

SEQUENCE FROM N.A.

SPECIES-Human;
MEDLING-9241214; PubMed-1326960;
MEDLING-92412144; PubMed-1326960;
Ras K., Michiels L., Merregaert J.;
Ras K., Michiels L., Merregaert J.;
"Genomic structure and expression of the human fau gene: er
"Genomic structure and expression of the human fau gene: er
"Inchies and expression of the human fau gene: er
"Inchies Res. Commun. 187:927-933(1992).

encoding

the

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; NCBI\_TaxID-9606, 10090, 10116, 10029, 9823; [1]

Hominidae;

Euteleostomi; Homo

scrofa (Pig).

SEQUENCE FROM N.A.

| O05472; O95261; O1-JUN-1994 (Rel. 29, Created) O1-JUN-1994 (Rel. 29, Last sequence update) O1-GCT-2001 (Rel. 40, Last annotation update) 40s ribosomal protein S30. FAU. Homo sapiens (Human), Mus musculus (Mouse), | ALIGNMENTS<br>SULT 1<br>30_HUMAN STANDARD; PRT; 59 AA. | 6 10.2 221 1 RS3A_PYRAE<br>6 10.2 233 1 YJO8_YEAST<br>6 10.2 235 1 CAV1_CAEEL | 6 10.2 219 1<br>6 10.2 220 1 | 6 10.2 211 1 T402_BURCE<br>6 10.2 217 1 KS1_HYDAT | 6 10.2 208 1 RISA_BUCAI<br>6 10.2 209 1 RHO1_YEAST | 10.2 208 1 RASM_MOUSE<br>10.2 208 1 RASM_RAT | 6 10.2 208 1 RASM_HUMAN |
|--|--|---|------------------------------|---|--|--|-------------------------|
|  |  | Q8zt21<br>P47006<br>Q94051  | P35536<br>P57280             | P24536<br>P38978                                  | P57212<br>P06780                                   | 008989<br>P97538                             | 014807                  |
|  |  |   | bacillus su<br>buchnera ap   | burkholderi<br>hydra atten                        | buchnera ap<br>saccharomyc                         | mus musculu<br>rattus norv                   | homo sapien             |

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EMBL; X65923; CAA46716.1; ALT_INIT.
EMBL; X6523; CAA46716.1; ALT_INIT.
EMBL; X62671; CAA44545.1; ALT_INIT.
EMBL; X65922; CAA46715.1; ALT_INIT.
EMBL; X65922; CAA46715.1; ALT_INIT.
EMBL; D36610; BAA05655.1; ALT_INIT.
EMBL; D3715; AAA91564.1; ALT_INIT.
EMBL; U31439; AAA83776.1; ALT_INIT.
EMBL; U4149; AAA857915.1; ALT_INIT.
EMBL; U712543; AAB55915.1; ALT_INIT.
EMBL; U712543; AAB5915.1; ALT_INIT.
EMBL; U712543; AAB5915.1; ALT_INIT.
                                                                                            P49689; 082203; Q9M0E4;
01-FEB-1996 (Rel. 33, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
405 ribosomal protein S30.
(RPS30A OR ATZG19750 OR F6F22.22) AND
(RPS30B OR AT4G29390 OR F17A13.210) AND
(RPS30C OR AT5G56670 OR MIK19.12).
                                                     Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
                                                                                                                                                                                                            _ARATH
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eurosids II; Brassicales; Bras
                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                   Ribosomal protein.
SEQUENCE 59 AA; 6648
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MGD; MGI:102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Ubiquitin is physiologically induced by interferons in luminal epithelium of porcine uterine endometrium in early pregnancy: global RT-PCR cDNA in place of RNA for differential display screening."; FEBS Lett. 405:148-152(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               between the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -I- MISCELLANEOUS: THIS RIBÓSOMAL PROTEIN IS SYNTHESIZED AS A C-TERMINAL EXTENSION PROTEIN (CEP) OF A UBIQUITIN-LIKE PROTEIN (SIMILARITY: BELONGS TO THE S30E FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97244440; PubMed=9089280; Chwetzoff S., D'Andrea S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPECIES-Pig;
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Submitted (DEC-1995) t
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Rossman T.G., Wang
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Genomics 25:291-294(1995).
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                                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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HGNC:3597; FAU.
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on of two retropseudogenes.";
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Pred. No. 2.2e-53;
Mismatches 0;
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RA Mayer K. F.X. Schueller C. Wambutt R., Murphy G., Volckaert G., Ra Pohl T., Duesterhoeft A., Stiekema W., Entlan K.-D., Terryn N., RA Pohl T., Duesterhoeft A., Stiekema W., Entlan K.-D., Terryn N., RA Pohl T., Duesterhoeft A., Stiekema W., Entlan K.-D., Terryn N., RA Pohl T., Duesterhoeft A., Stiekema W., Entlan K. P., Terryn N., RA Pohl T., Duesterhoeft A., Stiekema W., Bancroft I., RA Weichselgartner M., de Simone V., Obermaler B., Mache R., Mueller M., Radley P., RA Weichselgartner M., de Simone V., Obermaler B., Mache N., Bancroft I., RA Vos P., Hoheisel J., Zimmermann W., Wedler H., Radley P., RA Langham S.-A., McCullagh B., Bilham L., Robben J., RA Van der Schweren J., Grymonprez B., Chuang Y.-J., Vandenbussche F., RA Weitzenegger T., Bothe G., Ramsperger U., Hilbert H., Braun M., Weitzenegger T., Bothe G., Ramsperger U., Hilbert H., Braun M., Weitzenegger T., Bothe G., Ramsperger U., Hilbert H., Braun M., Rose M., Holtzer E., Brandt A., Peteters S., van Staveren M., Deltrise W., Rholtzer E., Brandt A., Peteters S., Van Staveren M., Deltrise W., Rholtzer E., Brandt A., Peteters S., Van Staveren M., Deltrise W., Rholtzer E., Brandt A., Peteters S., Van Staveren M., Deltrise R., Ra Weitzenegger T., Bothe G., Ramsperger U., Hilbert S., Peteter R., Buysshert C., Gielen J., Villarroel R., De Clercq R., Ra Pettett A., Rajandream M.A., Lyne M., Benes V., Rechmann S., Ra Pettett A., Rajandream M.A., Lyne M., Benes V., Rechmann S., Ra Pettett A., Rajandream M.A., Lyne M., Benes V., Rechmann S., Ra Borkova D., Bloecker H., Schmidt W., Grimm M., Loehnert T.-H., Ra Dose S., de Haan M., Maarse A.C. Schaefer M., Mueller A., Petavadi E., Ra Borkova D., Bloecker H., Schmidt W., Lecharny A., Aubourg S., Ra Median D., Haase D., Lemcke K., Mewest H.-W., Stocker S., Bielke C., Ra Marte M., Murray J., Sheet P., Cordes M., Abrines M., Habermann K., Petavan D., Lendardy T., Berton D., Kemp K., Lendardy A., Aubourg S., Bielke C., Ra Marte M., Berjotf A., Jones K., Donte M., Pepin K., Hillier L., Ra Gener V., Berton M., Joshu 
                       STRAIN=cv. Columbia;
MEDLINE=98403884; PubMed=9734815;
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Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D., Fujii C.Y., Mason T.M., Bownan C.L., Barnstead M.E., Feldblyum T.V., Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L., Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L., Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20083488; PubMed=10617198;
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           Nakamura
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                                                                                                                          N.A.
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30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
40S ribosomal protein S30.
FAU OR RPS30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-cv. Columbia; Shinozaki K., Davis R.W., Ecker J.R., Theologis A.; Shinozaki K., Davis R.W., Ecker J.R., Theologis A.; "RIKEN Arabidopsis full length cDNA clones (RAFLs) sequenced by t SSP consortium (Salk/Stanford/PGEC)."; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

1- SIMILARITY: BELONGS TO THE S30E FAMILY OF RIBOSOWAL PROTEINS.
                                                                                                             "An in situ hybridization screen for the rapid isolation of differentially expressed genes.";
Dev. Genes Evol. 210:28-33(2000).
-I- MISCELLANEOUS: THIS RIBOSOMAL PROTEIN IS SYNTHESTZED AS A C-TERMINAL EXTENSION PROTEIN (CEP) OF A UBIQUITIN-LIKE PROTEIN.
-I- SIMILARITY: BELONGS TO THE S30E FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                   Oryzias latipes (Medaka fish) (Japanese ricefish).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Meopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Beloniformes; Adrianichthyldae; Oryziinae; Oryzias.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Structural analysis of Arabidopsis thaliana chromosome 5. VI. Sequence features of the regions of 1,367,185 bp covered by 19 physically assigned Pl and TAC clones."; DNA Res. 5:203-216(1998).
                                                                                                                                                                                                                       MEDLINE=20070552; PubMed=10603084;
Henrich T., Wittbrodt J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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CONFLICT
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               the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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AL161574; CABP9697.; -.

L; AL109692; -; NOT_ANNOTATED_CDS.

L; AB013392; BAB99885.1; -.

L; AY052341; AAK96533.1; -.

L; AY061910; AAL31237.1; -.
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22; Conser
requires a license agreement (See http://www.isb-sib.ch/announce/
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Pred. No.
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QTP -> RHQ (IN REF. 1).
95D8F3EB72F53F33 CRC64;
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ng as its content is in no
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Matches 12
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Best Local Similarity
Matches 18; Conserv
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SEQUENCE
                                                                      042952; 014314;
15-DEC-1998 (Rel. 37, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
40S ribosomal protein S30.
40S ribosomal protein S30.
(RPS30A OR RPS30 OR SPAC19B12.04) OR (RPS30B OR SPBC19G7.03C).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gardner M.J., Tettelin H., Carucci D.J., Cummings L.M., Aravind L., Koonin E.V., Shallom S., Mason T., Yu K., Flylid C., Pederson J., Shen K., Jing J., Aston C., Lai Z., Schwartz D.C., Pertee M., Salzberg S., Zhou L., Sutton G.G., Clayton R., White O., Smith H.O. Fraser C.M., Adams M.D., Venter J.C., Hoffman S.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RS30_PLAFA 096269;
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                          Schizosaccharomyces pombe (Fission yeast Eukaryota; Fungi; Ascomycota; Schizosacc
                                                                                                                                                                                                                                                        SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RPS30 OR PFB0885W.
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30-MAY-2000 (Rel. 39, Last ann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmodium falciparum.
Eukaryota; Alveolata;
       Schizosaccharomycetales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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59 AA;
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58 AA; 6488 MW;
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RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamin N., Harris P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., McLean J.,
RA Holroyd S., Horls M., Leather S., McDonald S., McLean J.,
RA Rutherford K., Rutter S., Saunders D., Ouail M.A., Rabbinowitsch E.,
RA Ratherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Woodward J., Volkaert G., Aert R., Squares S., Stevens K.,
RA Woodward J., Volkaert G., Aert R., Robben J., Grymonprez B.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Hurtier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Gariutti L., Lowe T., McComble W.R., Paulsen I., Potashkin J.,
RA Gertutti L., Lowe T., McComble W.R., Paulsen I., Potashkin J.,
RA Gertutti L., Lowe T., McComble W.R., Paulsen I., Potashkin J.,
RA Gertutti L., Lowe T., McComble W.R., Paulsen I., Potashkin J.,
RA Gertutti L., Lowe T., McComble W.R., Paulsen I.,
RA Gertutti L., Excellent G., McComble W.R., Paulsen I.,
RA Gertutti L., Lowe T
                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 12; Conserv
               RS30_YEAST
Q12087;
Q1-NOV-1997
Q1-NOV-1997
Q1-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wood V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-21848401; PubMed=11859360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Transcription of ribosomal genes is down regulated starvation in fission yeast.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schizosaccharomyces
NCBI_TaxID-4896;
                                                                                                                                                              3 KVHGSLARAGKV 14
                                                                                                                                                                                              1 KVHGSLARAGKV
ribosomaı
                                                                                                                                                                                                                                                                                                                         AL390814; CAC00552.1; AL021839; CAA17057.2;
                                                                                                                                                                                                                                                                                                                                                            AJ002731; CAA05693.1; -.
                                                                                                                                                                                                                                                                                              protein;
61 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gwilliam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (NOV-1997) to the EMBL/GenBank/DDBJ databases
(Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 37, Last annotation update)
al protein S30.
                                                                                                                                                                                                                              Conservative
                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             æ.,
                                                                                                                                                                                                                                                                                              Multigene
6910 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (RPS30A AND RPS30B).
                                                                                                                                                                                                                                             20.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rajandream M.A., Lyne M., Lyne R.,
                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                           Score 12;
Pred. No.
                                                                                                                                                                                                                                                                                         family.
4B9C171F1A326F22 CRC64;
                                                                                                                                                                                                                              Mismatches
                                                                               62
                                                                                                                                                                                                                          1.4e-05;
hes 0;
                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                         Length 61;
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RESULT
RS30_ON
ID RS
ID RS
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GN FA
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Best Local
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EMBL; U48699; AAC49316.1; -.
EMBL; U83406; AAB41050.1; -.
EMBL; U83407; AAB41051.1; -.
EMBL; U17243; AAB67333.1; -.
EMBL; Z75090; CAA99391.1; -.
                                                                                                                                                                           RS30_ONCMY
P83328;
                                                                                 15-JUN-2002 (Rel. 41, Last sequence up 15-JUN-2002 (Rel. 41, Last annotation 40s ribosomal protein S30 (Fragment).
                                                                                                     15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last seg
15-JUN-2002 (Rel. 41, Last ann
  Eukaryota; Metazoa; Actinopterygii; Neop
                                          Oncorhynchus mykiss
                                                                                                                                                                                                                        ONCMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hughes B., Pohl T.M.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
-i- MASS SPECTROMETRY: MW-6987; MW_ERR-3.4; METHOD-MALDI.
-i- MISCELLANEOUS: THERE ARE TWO GENES FOR S30 IN YEAST.
-i- SIMILARITY: BELONGS TO THE S30E FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Favello A., Fulton L., Gattung S., Greco T., Kirsten J., K Hallsworth K., Hawkins J., Hillier L., Jier M., Johnson D., Johnston L., Langston Y., Latreille P., Le T., Mardis E., Miller N., Nhan M., Pauley A., Peluso D., Riken L., Riles Taich A., Trevaskis E., Vignati D., Wilcox L., Wohldman P., Submitter A., Naterston R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content modified and this statement is not removed. Usage by ar entities requires a license agreement (See http://www.isb-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ribosomal protein; Multigene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (RPS30B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Baker R.T., Williamson N.A., Wettenhall R.E.H.;
"The yeast homolog of mammalian ribosomal protein S30 is expressed from a duplicated gene without a ubiquitin-like protein fusion sequence. Evolutionary implications.";
J. Biol. Chem. 271:13549-13555(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (RPS30A OR YLR28/BC OR LUVUILLE, Saccharomyces cerevisiae (Baker's yeast).
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycetas; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-96278780;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND SEQUENCE (RPS30A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                              N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S0004278; RPS30A.
S0005708; RPS30B.
                                                                                                                                                                                                                                                                                                            KVHGSLARAGKV
                                                                                                                                                                                                                                                                                                                                                                                               l Similarity
12; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA;
                                                                                                                                                                                                  STANDARD;
20a; Chordata;
Neopterygii; 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed-8662789;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6987 MW;
(Rainbow trout) (Salmo gairdneri)
Chordata; Craniata; Vertebrata; E
pterygil; Teleostei; Euteleostei;
                                                                                                                                                                                                                                                                                                                                                                                         100.08; F1
                                                                                                                                                                                                                                                                                                                                                                                                                                          20.3%;
                                                                                                                                                                                                                                                                                                                                                                                                               Score 12; ; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65EADAED8D9FC586 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            family.
                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                       update)
                                                                                                                                                                                             11
                    Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                 1.4e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Johnson D.,
Mardis E., Menezes S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Riles L.
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tent is in
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CO1B_HUMAN
09BR76;
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Q09261;
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Matches
                                                                                             RESULT 9
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FEBS Lett. 244:34-38(1989).

FEBS Lett. 244:34-38(1989).

FEBS Lett. 244:34-38(1989).

FEBS Lett. 244:34-38(1989).

FRABILITY AND INHIBITS TIGHTLY TO DS-DNA, INCREASES ITS THERMAL STABLITY AND INHIBITS TRANSCRIPTIONAL TREGULANOR THROUGH ITS FOUNCTION. MAY BE A GLOBAL TRANSCRIPTIONAL REGULANOR THROUGH ITS ABILITY TO BIND TO CURVED DNA SEQUENCES, WHICH ARE FOUND IN REGIONS UPSTREAM OF A CERTAIN SUBSET OF PROMOTERS. IT PLAYS A ROLE IN THE THERMAL CONTROL OF PILI PRODUCTION. IT IS SUBJECT TO TRANSCRIPTIONAL AUTO-REPRESSION. IT BINDS PREFERRNIALLY TO THE UPSTREAM REGION OF ITS OWN GENE RECOGNIZING TWO SEGMEMYS OF DNA ON BOND SCONTILL TO THE DAYS AND SEGMEMYS OF DNA ON BOND SCONTILL TO THE DAYS AND SEGMEMYS OF DNA ON BOTHER RECOGNIZING TWO SEGMEMYS OF DNA ON BOTHER DAYS OF DNA ON BETTER THE DAYS AND SEGMEMYS OF DNA ON BOTHER DAYS OF DNA ON THE DAYS OF 
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                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                            Fernandes J.M.O., Smith V.J.; "A novel antimicrobial function for a ribosomal peptide from skin secretions of rainbow trout.";
                                                                                                                                                                                                                                      -1- MASS SPECTROMETRY: MW-6676.6; METHOD-MALDI.
-1- SIMILARITY: BELONGS TO THE S30E FAMILY OF RIBOSOMAL PROTEINS.
Ribosomal protein; Antibiotic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- SUBUNIT: HOMODIMER.
-1- SUBUNIT: HOMODIMER.
-1- SUBUNIT: BELONGS TO THE HISTONE-LIKE PROTEIN H-NS FAMILY.
PIR; S02776; S02776.
HSSP; P08936; JHNR.
InterPro; IPR001801; Histone HNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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                                                                                                                                                                           Submitted (APR-2002) to the SWISS-PROT data bank.
Protacanthopteryg11; Salmoniformes; Salmonidae; Oncorhynchus. NCBI_raxID=8022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 133;
                                                                                                                                                                                                                                                                                                                                                              18.6%; Score 11; DB 1; Length 11; 100.0%; Pred. No. 3.4e-05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1990 (Rel. 16, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
DNA-binding protein H-NS (Histone-like protein HLP-II).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  133 AA; 15134 MW; B92C49F7995C5ED5 CRC64;
                                                                                                                                                                                                                                                                                                   NON_TER 11 11 23 MW; 2312AB630DD735B8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA-binding; Transcription regulation; Repressor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.9%; Score 7; DB 1;
100.0%; Pred. No. 3.3;
ive 0; Mismatches
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                                                                       FUNCTION, AND MASS SPECTROMETRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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ProDom; PD007337; Histone_HNS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Rel. 16, Created)
                                                                                                                                                                                                                                                                                                                                                                18.6%;
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Best Local Similarity 100...
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                           TISSUE-Skin mucus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proteus vulgaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=585;
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01-NOV-1990
01-NOV-1995
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P18818;
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SEQUENCE
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                                                                                                                                                                                 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -:- FUNCTION: MAY BE INVOLVED IN CYTOKINESIS, MOTILITY, AND SIGNAL TRANSDUCTION (BY SIMILARITY).
-:- SUBUNIT: BINDS ACTIN (BY SIMILARITY).
-:- SIMILARITY: CONTAINS 5 WD REPEATS (TRP-ASP DOMAINS).
-:- SIMILARITY: BELONGS TO THE CORONIN FAMILY OF WD-REPEAT PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                           01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 39.2 kba protein C32A3.2 in chromosome III.
                                                                                                                                                                                                                                                                                                                          Thomas K.;
Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D511225F5062B420 CRC64;
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Coronin 1B (Coronin 2).
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100.0%; Pred. No. 7.5
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein.
SEQUENCE 346 AA; 39221 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last seq
15-JUN-2002 (Rel. 41, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; 248241; CAA88285.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WormPep; C32A3.2; CE01506.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 100.
nes 7; Conservative
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                         Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Placenta;
                                                                                                                                                                                                                             NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
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and for commercial
                                            (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MECLINE-93187617; PubMed-8445371; Sneider J.M., Kinney R.M., Tsuchiya K.R., Trent D.W.; Sneider J.M., Kinney R.M., Tsuchiya K.R., Trent D.W.; Sneider J.M., Kinney R.M., Tsuchiya K.R., Trent D.W.; Molecular evidence that epizootic Venezuelan equine encephalitiss (VEE) 1-AB viruses are not evolutionary derivatives of enzootic VEE subtype I-E or II viruses...; J. Gen. Virol. 74:519-523(1993).

I. FUNCTION: THE CAPSID PROTEIN IS AN AUTO-PROTEASE.

I- FUNCTION: THE CAPSID PROTEIN CLEAVAGES IN VIVO YIELD MATURE PROTEINS.

I- PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.

I- MISCELLANBOUG: THE 6 kDa POLYPEPTIDE PROBABLY SERVES AS THE SIGNAL SEQUENCE FOR THE MEMBRANE GLYCOPROTEIN E1, WHICH IS THE VIRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POLS_EEVVM STANDARD; PRT; 1254 AA.
POLS_EEVVM STANDARD; 066589; 066590; 066591;
01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
5Kructural polyprotein (Pl30) [Contains: Coat protein C (EC 3.4.21.-)
(Capsid protein C); Spike glycoprotein E3; Spike glycoprotein E2;
6 kDa peptide; Spike glycoprotein E1].
Venezuelan equine encephalitis virus (strain Mena II).
Viruses; SSRNA positive-strand viruses, no DNA stage; Togaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 489;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                   Usage by
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A6012FDA683ECB59 CRC64;
                                                                                                                                                 Genew; HGNC:2253; COROIB.,
InterPro; IPR001680; WD40.
Pfam; PF00400; WD40; 3.
ProDom; PD000018; WD40; 1.
SWART; SM00320; WD40; 3.
PROSITE; PS00678; WD_REPEATS_1; 1.
PROSITE; PS50082; WD_REPEATS_2; 2.
PROSITE; PS50294; WD_REPEATS_2; 2.
ACLID-binding; Repeat; WD repeat; Coiled coil.
modified and this statement is not removed. entities requires a license agreement (See lor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.9%; Score 7; DB 1
100.0%; Pred. No. 10;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; AAA42989.1; ALT_TERM.
; AAA42991.1; ALT_SEQ.
; AAA42992.1; ALT_SEQ.
; AAA42993.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                               MD 2.
MD 2.
MD 4.
                                                                                                                        EMBL; BC006449; AAH06449.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54234 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             489 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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442 GSLARAG 448
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L04599;
L04599;
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POLS_EEVVM
DCLS_EEVVM
DT 01-JUN-
DT 01-JUN-
DE (Capsito
CC VITUSEC

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                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                           Coat protein; Polyprotein; Transmembrane; Glycoprotein; Hydrolase;
Serine protease.
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CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                (GLCNAC. . .) (POTENTIAL).
(GLCNAC. . .) (POTENTIAL).
(GLCNAC. . .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
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01-APR-1990 (Rel. 14, Last sequence update)
01-FBB-1996 (Rel. 32, Last annotation update)
40S xibosomal protein $27a.
Dictyostelium discoideum (Slime mold).
Eukaryota: Mycetozoa; Dictyostelium.
                                                                                                                                                                                             SPIKE GLYCOPROTEIN E3.
SPIKE GLYCOPROTEIN E2.
6 KDA PEPTIDE.
SPIKE GLYCOPROTEIN E1.
                                                                                                                                                                                                                                                                                                       N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
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. 22;
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                                         InterPro; IPR002548; Alpha_El_glycop.
InterPro; IPR000936; Alpha_E2_glycop.
InterPro; IPR000936; Alpha_E2_glycop.
InterPro; IPR001836; Alpha_core.
InterPro; IPR000930; Togavirin.
Pfam: PF00943; Alpha_E2_glycop; 1.
Pfam: PF01563; Alpha_Core; 1.
Pfam: PF01563; Alpha_E3_glycop; 1.
Pfam: PF01563; Alpha_E3_glycop; 1.
Pfam: PF01563; Alpha_E1_glycop; 1.
                                                                                                                                                                                                                                                                                  POTENTIAL. POTENTIAL.
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                                                                                                                                                                                                                                                            CHARGE REI
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                     Score 7;
EMBL; L04599; AAA42994.1; ALT_INIT.
PIR; JQ1979; JQ1979.
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100.08; Fi
                                                                                                                                                                                                                                                                                                                                                               138343 MW;
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hes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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333
756
812
1254
151
157
225
721
813
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                       P03315; 1VCP
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                                                                                                                                                                                                                                                                                                                                                  946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=44689
                                                                                                                                                                                                                                                                                             1231
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ACT_SITE
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TRANSMEM
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R27A_DICDI
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EX7S_VIBCH
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A Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,

RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,

RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,

RA Chim S.Y., Claser P., Goffeau A., Galitty E.J., Grandi G.,

RA Guiseppi G., Guy B.J., Haga K., Haiceh J., Harwood C.R., Henaut A.,

RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,

RA Kuria K., Lapidus A., Liu H., Masuda S., Mauel C., Medigue C.,

RA Kurita K., Lapidus A., Liu H., Masuda S., Mauel C., Medigue C.,

RA Modina N., Mellado R.P., Koningstein G., Krogh S., Kumano M.,

RA Modina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,

RA Presecan E., Pujic P., Purnelle B., Rosonilik S., Persocott A.M.,

RA Presecan E., Pujic P., Purnelle B., Rose M., Sadaie Y.,

RA Presecan E., Scallan E., Schleich S., Schroeter R., Scallan E., Scallan E., Scallan E., Scallan E., Scallan E., Scallan E., Schleich S., Schroeter R., Sato T., Scallan E., Schleich S., Schroeter R., Scallan E., Scallan E., Scallan E., Rose M., Sato T., Scallan S., Nandelle M., Vandenbol M., Vandenbol M., Vasanoto K., Yata K.,

RA Tosato V., Uchiyama S., Vandenbol M., Vannier R., Yasumoto K., Yata K.,

Minters P., Walder E., Wedler 
                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ogasawara N., Nakai S., Yoshikawa H.; "Systematic sequencing of the 180 kilobase region of the Bacillus subtilis chromosome containing the replication origin.";
                                                                                                                                                                                                                                                                                               ó,
                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus. NCBL_TaxID=1423;
                                                 DictyDb; DD010/20; InterPro: INTERPRO/102906; Ribosomal_S27.
InterPro: IPR002906; Ribosomal_S27; 1.
Ribosomal protein; Zinc-finger; Metal-binding.
LYS-RICH (HIGHLY BASIC).
                                                                                                                                                                                               F77B3E09D1B7246F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-1991 (Rel. 18, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
30S_ribosomal protein S18 (BS21).
                                                                                                                                                                                                                                              Score 6; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78 AA.
                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                        Pred. No.
EMBL; M23750; AAA33264.1; ALT_INIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-96051385; PubMed-7584024;
                                                                                                                                                                                                                                                                     100.08;
                                                                                                                                                                   ZN_FING 46 69
SEQUENCE 78 AA; 8915 MW;
                                                                                                                                                                                                                                              10.2%;
                                                                                                                                                                                                                                                                                               6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA Res. 1:1-14(1994).
                  PIR; E34080; UQDOR7
D1ctyDb; DD01026; -
                                                                                                                                                                                                                                                                     Local Similarity
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                           24 KKKKKT 29
                                                                                                                                                                                                                                                                                                                                                                        4 KKKKKT 9
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P21475;
                                                                                                                                                                                                                                              Query Match
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ID R318_BACSU
R718_BACSU
R718_BACSU
DT 01-MAY.
DT 01-MAY.
DT 01-MAY.
DT 01-MAY.
DE 30S r118
GN RESIN.
GN NEBL.
GN NEBL.
RR SEQUEN
RR STAIN.
RA ACCOCK
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MEDLINE=20406833; Pubbled=10952301;
MEDLINE=20406833; Pubbled=10952301;
Medelberg J.F., Eisen J.A., Hack DI., Haft DI., Tettelin H., Richardson D., Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragol I., Sellers P., McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- FUNCTION: BIDIRECTIONALLY DEGRADES SINGLE-STRANDED DNA INTO LARGE ACID-INSOLUBLE OLIGONUCLEOTIDES, WHICH ARE THEN DEGRADED FURTHER
                                                                                                                                                                                                                          Mol. Gen. Genet. 185:239-244(1982).
-!- FUNCTION: This protein has been implicated in aminoacyl-transfer
RNA binding. It appears to be situated at the decoding site of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                               SEQUENCE OF 1-23.
SEQUENCE OF 1-23.
MEDLINE-82219212; PubMed-6806564;
Higo K.I., Otaka E., Osawa S.;
Higo K.I., Otaka E., Osawa S.;
"Purification and characterization of 30S ribosomal proteins from "Purification and characterization of Bacherichia coli 30S proteins.";
Bacillus subtilis: correlation to Escherichia coli 30S proteins.";
Genet. 185:239-244(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                   -1- SIMILARITY: BELONGS TO THE S18P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA sequence of both chromosomes of the cholera pathogen Vibrio
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16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Probable exodeoxythobonuclease VII small subunit (EC 3.1.11.6)
(Exonuclease VII small subunit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78 AA; 8838 MW; 1CF19CE039C64FF2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfan; PF01084; Ribosomal_S18; 1.
PRINTS; PR00974; RIBOSOMALS18.
TODOM; PD002239; Ribosomal_S18; 1.
TIGRFAMS; TIGROOU165; S18; 1.
PROSITE; PS00057; RIBOSOMAL_S18; 1.
Ribosomal protein; RNA-binding; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Pred. No. 22; ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.2%; Score 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; D26185; BAA05219.1; ALT_INIT.
EMBL; Z99124; CAB16126.1; ALT_INIT.
PIN; S11368, S11368.
Subtilist; BG10047; rpsR.
InterPro; IPR001648; Ribosomal_S18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 406:477-483(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
Nature 390:249-256(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vibrio cholerae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           XSEB OR VC0891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30 GRAKRR 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EX7S_VIBCH Q9KTL1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INIT_MET
SEQUENCE
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11 SLARAG 16

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RESULT 16
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                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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SMALL ACID-SOLUBLE OLIGONUCLEOTIDES (BY SIMILARITY).
                                                 -!- CATALYTIC ACTIVITY: Exonucleolytic cleavage in either 5'- to 3'-
or 3'- to 5'-direction to yield nucleoside 5'-phosphates.
-!- SUBUNIT: HETEROOLIGOMER COMPOSED OF LARGE AND SMALL SUBUNITS (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein in grm 3'region (Fragment).
Micromonospora echinospora (Micromonospora purpurea).
Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
Actinomycetales; Micromonosporineae; Micromonosporaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-91192615; PubMed-2013410;
Kelemen G.H., Cundliffe E., Financsek I.;
"Cloning and characterization of gentamicin-resistance genes from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 80;
                                                                                                                                                          -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         105 AA; 11111 MW; 0B398039381DB012 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF02609; Exonuc_VII_S; 1.
TIGRFAMs; TIGR01280; xseB; 1.
Hydrolase; Nuclease; Exonuclease; Complete proteome.
SEQUENCE 80 AA; 8911 MW; F9B7F5A9C6821DD1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Micromonospora purpurea and Micromonospora rosea.", Gene 98:53-60(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.2%; Score 6; DB 1;
100.0%; Pred. No. 28;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
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100.0%; Pred. No. ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                105 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nterPro; IPR003761; Exonuc_VII_S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE004173; AAF94053.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M55520; AAA25337.1; -
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Best Local Similarity
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Best Local Similarity
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                                                                                                                                 SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VC0891;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YGRM_MICEC
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YGRM_MICEC
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5 SLARAG 10

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                               Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
Actinomycetales; Micromonosporineae; Micromonosporaceae;
                                                                                                                                                                                                                                                                                            Kelemen G.H., Cundliffe E., Financsek T.;
Cloning and characterization of gentamicin-resistance genes from
Micromonospora purpurea and Micromonospora rosea.";
Gene 98:53-60(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Treponema pallidum.
Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
                                                            01-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein in GRM 3'region (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.2%; Score 6; DB 1;
100.0%; Pred. No. 28;
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antibiotic resistance, Hypothetical protein.
105 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123 AA
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MEDLINE-98332770; PubMed-9665876;
                                                                                                                                                                                                                                                                             MEDLINE=91192615; PubMed=2013410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Rel. 37, Created)
                                           (Rel. 21, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M55521; AAA25339.1; -. PIR; PW0018; PW0018.
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  STANDARD;
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                                                                                                                             Micromonospora rosea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                              NCBI_TaxID=1878;
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                                                                                                                                                                                          Micromonospora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 SLARAG 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-OCT-2001 (F
50S ribosomal
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                                         01-MAR-1992
                                                            01-FEB-1996
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 SLARAG
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083879;
  YGRM MICRO
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SEQUENCE
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4 GSLARA 9
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81 GSLARA
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9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
               FUNCTION: THIS PROTEIN IS LOCATED AT THE 30S-50S RIBOSOWAL SUBUNIT INTERFACE AND MAY PLAY A ROLE IN THE STRUCTURE AND FUNCTION OF THE AMINOACYL-TRNA BINDING SITE (BY SIMILARITY).

SIMILARITY: BELONGS TO THE L19P FAMILY OF RIBOSOWAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Cloning and sequencing a cDNA encoding human ribosomal protein S25."; Gene 107:329-333(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
Makaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606, 10090, 10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-21864036; PubMed-11875025;
Yoshihama M., Uechi T., Asakawa S., Kawasaki K., Kato S., Higa Maeda N., Minoshima S., Tanaka T., Shimizu N., Kenmochi N.;
"The human ribosomal protein genes: sequencing and comparative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.2%; Score 6; DB 1; Length 123;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                  TIGR; TP0909; -.
InterPro; IPR001857; Ribosomal_L19.
Pfam; PF01245; Ribosomal_L19; 1.
PR.NTS; PR00061; RIBOSOMALL19.
ProDom; PD002979; Ribosomal_L19; 1.
PTGREAMS; TIGR01024; PDLS_Dact. 1.
PROSITE; PS01015; RIBOSOMAL_L19; 1.
RIBOSOMAL_L19; 1.
RIBOSOMAL_L19; 1.
RIBOSOMAL_L19; AM; 123E652CB4B545EF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Pred. No. 32;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPECIES-Human; TISSUE-Pancreas, and Skin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-92084127; Pubmed-1748303;
L1 M., Latoud C., Center M.S.;
"Cloning and sequencing a CDNA end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
SPECIES-Mouse; STRAIN-C57BL/6J;
                                                                                                                                                                                                                                                                                                  EMBL; AE001259; AAC65861.1; -.
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01-MAY-1992 (Rel. 22, Last seq
15-JUN-2002 (Rel. 41, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      analysis of 73 genes.";
Genome Res. 12:379-390(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40S ribosomal protein S25.
RPS25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse), and
Science 281:375-388(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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89 RAGKVR 94
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ID RS25_HUMAN
ID RS25_HUMAN
ID T 01-MAY.
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Arakwa T., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakwa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Arakwa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Alzawa K., Izawa M., Nishi Y., Konno H., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukwa T., Saito R.,
Kadota K., Matsuda H.A., Ashburnar M., Batalov S., Casawant T.,
Relischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.
Kueli P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Sakai K., Okido T., Furuno M., Aono H., Balarelli R., Barsh G.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Ronstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Nordone P., Ring B., Ringwald M., Rodityuez I., Sakameto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibate Y., Storch K.-F.,
Wynshw-Boolis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
M. Washiyaki V.
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Biochem. Biophys. Res. Commun. 186:1688-1693(1992).
-!- SIMILARITY: BELONGS TO THE S25E FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
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MEDLINE-92378645; PubMed-1354961;
Chan Y.-L., Wool I.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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100.0%; Pred. No. 33;
ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGD; MGI:1922867; Rps25.
InterPro; IPR004977; Ribosomal_S25.
Pfam; PF03297; Ribosomal_S25; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AB061844; BAB79482.1; --
EMBL; BC003537; AAH03537.1; --
EMBL; BC004294; AAH04294.1; --
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EMBL; AK012696; BAB28417.1; -
EMBL; BC002088; AAH02088.1; -
EMBL; X62482; CAA44349.1; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 409:685-690(2001).
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Best Local Similarity
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MEDLINE=96109932; PubMed=8619318;
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Best Local Similarity
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                                                                                                                                                                                 24 KKKKKT 29
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84 KKKKT
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P53908;
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                                                                                                                                                                                                                                                         FUNCTION: SII PLAYS AN ESSENTIAL ROLE FOR THE SELECTION OF THE CORRECT TRNA IN PROTEIN BIOSYNTHESIS. IT IS LOCATED ON THE LARGE LOBE OF THE SMALL SUBUNIT (BY SIMILARITY).
SIMILARITY: BELONGS TO THE SIIP FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID=6239;
                                                                                                                                                                     MEDLINE-99039499; PubMed-9823893; Andersson J.O., Andersson S.G.E., Zomorodipour A., Andersson J.O., Sicheritz-Ponten T., Alsmark U.C.M., Pondowski R.M., Naeslund A.K., Eriksson A.-S., Winkler H.H., Kurland C.G.; The genome sequence of Rickettsia prowazekii and the origin of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                 Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettslaceae; Rickettsleae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ribosomal protein; Complete proteome.
SEQUENCE 127 AA; 13583 MW; BED96964C891616C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 13.7 kDa protein C18H9.2 in chromosome II.
C18H9.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                      Last sequence update)
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     127 AA
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Pfam; PF00411; Ribosomal_S11; 1.
ProDom; PD001010; Ribosomal_S11; 1.
PROSITE; PS00054; RIBOSOMAL_S11; FALSE_NEG.
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                       30-MAY-2000 (Rel. 39, Creat 30-MAY-2000 (Rel. 39, Last 16-CCT-2001 (Rel. 40, Last 30S ribosomal protein S11. RPSK OR RF636.
                                                                                                                                                                                                                                              Nature 396:133-140(1998).
  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Conservative
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                                                                                      Rickettsia prowazekii.
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                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                          NCBI_TaxID-782;
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                                                                                                                                                                                                                                    mitochondria.
 RS11_RICPR
092CS8;
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Q09237;
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A 43.5 Kb segment of yeast chromosome XIV, which contains MFA2,
MEP2, CAP/SRV2, NAM9, FKB1/FPR1/RBP1, MOM22 and CPT1, predicts an
adenosine deaminase gene and 14 new open reading frames.";
Yeast 11:1195-1209(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomycetes;
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01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
Hypothetical 15.3 kDa protein in MFA2-MEP2 intergenic region.
YNL143C OR N1206 OR N1795.
Saccharomyces cerevistae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycetusets
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Last annotation update)
Protein in IXRI-TFA1 intergenic region.
                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 130;
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                                                                                                                        EMBL; U23147; AAC46687.1; -. WormPep; C18H9.2; CE01802. Hypothetical protein. SEQUENCE 128 AA; 13666 MW; C7A64D960B95E2EC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; 246843; CAA86683.1; -.
EMBL; 271419; CAA96026.1; -.
SGD; S0005087; YNL143C.
Hypothetical protein: SEQUENCE 130 AA; 15319 MW; 29070E47FC63436D CRC64;
                                                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.2%; Score 6; DB 1;
100.0%; Pred. No. 34;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      130 AA.
                                                                                                                                                                                                                                                                                    100.0%; Pred. No. 33;
live 0; Mismatches
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                                                                                                                                                                                                                                                                    Score 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Rel. 29, C
(Rel. 29, I
(Rel. 32, I
1 15.6 kDa F
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ID YKD1_Y
AC P36098
DT 01-JUN
DT 01-JUN
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DE HYPOTH
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                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (RPS16A).
STRAIN-S28BC / AB972;
Badcock K., Churcher C., Barrell B.G., Rajandream M.A., Walsh S.V.;
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RS16_YEAST STANDARD; PRT; 142 AA.
P40213; P26787;
01-A0G-1992 (Rel. 31, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
40S ribosomal protein S16 (RP61R).
(RPS16A OR RP61R OR YMR143W OR YM9375.12) AND (RPS16B OR YDL083C).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi, Ascomycota; Saccharomycotina, Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-92184799; PubMed-1544921;
Takakura H., Tsunasawa S., Miyagi M., Warner J.R.;
"NH2-terminal acetylation of ribosomal proteins of Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Biol. Chem. 267:5442-5445(1992).
-!- MISCELLANEOUS: THERE ARE TWO GENES FOR S16 IN YEAST.
-!- SIMILARITY: BELONGS TO THE S9P FAMILY OF RIBOSOMAL PROTEINS.
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                                                                                                                                                                                                                                                     Length 142;
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Wambutt R., Wedler H., Wedler E., Scharfe M.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                        142 AA; 15739 MW; 19408A7791FF4356 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15873374B3262144 CRC64;
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Probom; PD01627; Ribosomal_S9; 1.
PR051TF; PS00360; RibosomAL_S9; 1.
Ribosomal protein; Acetylation; Multigene family.
                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
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Pred. No.
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EMBL; 274131; CAA98649.1; -.
EMBL; 270131; RAS16A.
SGD; S0002751; RPS16B.
InterPro; IPR000754; Ribosomal_S9.
                                                      Pfam; PF00380; Ribosomal_S9; 1.
ProDom; PD001627; Ribosomal_S9; 1.
PROSITE; PS00360; RIBOSOMAL_S9; 1.
                         InterPro; IPR000754; Ribosomal_S9
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      EMBL; AL033497; CAA21965.1;
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                                                                                                                                                                                                                                                                                                                  Conservative
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                    Ribosomal protein.
                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID-4932;
                                                                                                                                                                                                                                                                                                                                                                         48 TFGKKK 53
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                                                                                                                                                                                                                                                     Query Match
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RS16_YEAST
                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as its connect to the modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                        Purnelle B., Skala J., van Dyck L., Goffeau A.;
"Analysis of an 11.7 kb DNA fragment of chromosome XI reveals a new tRNA gene and four new open reading frames including a leucine zipper protein and a homologue to the yeast mitochondrial regulator ABF2."; Yeast 10:125-130(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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16-0CT-2001 (Rel. 40, Last annotation update)
40S ribosomal protein S16.
RPS16 OR CA49C10.01C.
Candida albicans (Yeast)
Eukaryota; Fung1; Ascomycota; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
                         Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Taylor K., Harris D., Barrell B.G., Rajandream M.A.;
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
-1- SIMILARITY: BELONGS TO THE S9P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
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82908E65C7E37CFC CRC64;
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EMBL; 228031; CAA81866.1; -.
PIR; S37848; S37848.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transmembrane
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                                                                                                                                                                                                                                           MEDLINE-94262309; PubMed-8203146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  113 129 PC
137 AA; 15626 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001 (Rel. 40, Created)
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Hypothetical protein; T
TRANSMEM 36 52
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YKL031W OR YKL244.
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094017;
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SEQUENCE
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ID RS16_C

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143 EKKKKK 148
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RPL14 OR LPD23.
 AGKVRG 14
                    AGKVRG 55
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Q25278;
                                                                           YK20_YEAST
P36133;
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                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the ENBL cutstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a licensee agreement (see http://www.isb-sib.ch/announce/or send an email to licenseelab-sib.ch).
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                                                                                                                                                                                                                                                     "Nucleotide sequence and primary structures of gene products coded for by the T4 genome between map positions 48.266 kb and 39.166 kb."; Nucleic Acids Res. 15:3632-3633(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                           MEDLINE-89065345; PubMed-2974005; Barth K.A., Powall D., Trupin M., Mosig G.; Barth K.A., Fowall D., Trupin M., Mosig G.; Regulation of two nested proteins from gene 49 (recombination endonuclease VII) and of a lambda RexA-like protein of bacteriophage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfan; PF02945; endonuclease_7; 3.
Hydrolase; Endonuclease; Nuclease; Alternative initiation.
CHAIN 1 157
RECOMBINATION ENDONUCLEASE VII, LONG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1- ALTERNATIVE PRODUCTS: 2 isoforms are produced by alternative
                                                                                                                                                                                                                                                                                                                                                                                     Bacteriophage T4.
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
T4-like viruses.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RECOMBINATION ENDONUCLEASE VII,
                                                                        END7_BPT4 STANDARD; PRT; 157 AA.
P13340; Q38426; Q9T0V4;
P1340-1390 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Recombination endonuclease VII (EC 3.1.-.) (Protein GP49).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FOR SHORT ISOFORM,
86233D2A7FC0F9A8 CRC64;
                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND ALTERNATIVE INITIATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100.0%; Pred. No. 40; Matches 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.2%; Score 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; Y00122; CAA68307.1; --
EMBL; AF158101; AAD42477.1; --
EMBL; AF158101; AAD42687.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ISOFORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR004211; Endonuclease_7.
                                                                                                                                                                                                                              MEDLINE-87203398; PubMed-3575111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53 FC
18144 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X12629; CAA31148.1; -. EMBL; X12629; CAA31149.1; -.
                                                                                                                                                                                                                                           Comaschewski J., Rueger W.;
                                                                                                                                                                                                                                                                                                                                                                  Genetics 120:329-343(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        HETERODUPLEX LOOPS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; A30291; ZNBPT9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53
157 AA;
                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                     NCBI_TaxID=10665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              initiation.
48 TFGKKK 53
                    8 TFGKKK 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hydrolase; E
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INIT_MET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
                                                      RESULT 25
                                                                 END7_BPT4
                    qq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Campos-Neto A., Soong L., Cordova J.L., Sant'Angelo D., Skeiky Y.A.W., Ruddle N.H., Reed S.G., Janeway C. Jr., McMahon-Pratt D.; Red S.G., Janeway C. Jr., McMahon-Pratt D.; Red S.G. a Leishmania donovani gene instructed by a peptide isolated from major histocompatibility complex class II molecules of infected macrophages."; J. Exp. Med. 182:1423-1433(1995).

- STMILARITY: BELONGS TO THE LIJE FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Leishmania donovani.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
                                                                                                                                                                                                                Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Probable 40S ribosomal protein L14 (23 kDa cell surface protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                           Last sequence update)
Last annotation update)
protein in GAP1-NAP1 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                          Urrestarazu L.A., Jauniaux J.-C.;
Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LYS-RICH (HIGHLY BASIC).
51BC98B657A720C2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
167 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                175 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.2%; Score 6; DB 1
100.0%; Pred. No. 42;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-96042140; PubMed-7595213;
                                                       01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last seq
15-DEC-1998 (Rel. 37, Last ann
Hypothetical 19.2 kDa protein i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  144 167 L
167 AA; 19222 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; Z28265; CAA82114.1; -. EMBL; Z28266; CAA82117.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; 228266; CAA82117.1
PIR; S38112; S38112.
SGD; S0001748; YKR040C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein.
DOMAIN 144 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=4932;
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SEQUENCE FROM N.A.
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                                                  DEVELOPMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HIIIII
RGQTPK 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CC42_CAEEL
Q05062;
                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                              SIGNAL
                                                                                                                                                                                                                                                                                                                                                             CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 29
   6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arakawa T., Hara A., Shibata K., Yoshino M., Itch M., Ishii Y., Arakawa T., Hara A., Shibata K., Yoshino M., Itch M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Alaawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Golobori T., Bono H., Kasukawa T., Saito R., Ashburner M., Batalov S., Casavant T., Ridota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Richi F., Lewis S., Matsuo Y., Nikaldo I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Sizuki R., Tomita M., Wagner L., Washio T., Ashai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Asakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Asakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Abrownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchlonni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakameto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Whitmay H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wanshaw-Boolis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
FXVD domain-containing ion transport regulator 5 precursor (Oncoprotein-Induced protein 2) (Ion channel homolog RIC) (EF-8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fu X., Kamps M.P.;
"E2a-Pbx1 induces aberrant expression of tissue-specific a
developmentally regulated genes when expressed in NIH 3T3
                                                                                                                                                                                                                                                                             Length 175;
                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                             175 AA; 19887 MW; A3F9AFF30D986814 CRC64;
                                                                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                                                                                 10.2%; Scor.
100.0%; Pred. No. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                            178 AA.
                                                                                                                                            EMBL; X86551; CAA60246.1; -.
InterPro; IPR000302; KOW_motif.
InterPro; IPR002784; Ribosomal_L14e.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cell. Biol. 17:1503-1512(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-C57BL/6J; TISSUE-Spleen;
MEDLINE-21085660; Pubmed-11217851;
                                                                                                                                                                                            Pfam; PF00467; KOW; 1.
Pfam; PF01929; Ribosomal_L14e; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-97184476; PubMed-9032278;
                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         musculus (Mouse)
                                                                                                                                                                                                                              Ribosomal protein.
SEQUENCE 175 AA;
                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                              160 AKRRMQ 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                            32 AKRRMQ 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-BALB/C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FXYDS OR OIT2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fibroblasts."
                                                                                                                                                                                                                                                                                                                                                                                                                                                       FXYS_MOUSE
P97808;
                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-93293845; PubMed-8514766; Chen W., Lim H., Lim L.; The CDC42 homologue from Caenorhabditis elegans. Complementation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE SMALL GIPASE SUPERFAMILY. RHO FAMILY.
-i- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
-i- TISSUE SPECIFICITY: SPLEEN, LUNG, SKELETAL MUSCLE, AND TESTIS.
-i- DEVELOPMENTAL STAGE: EXHIBITS BIPHASIC EXPRESSION DURING
                                                                                                                                                                                                                                                                                                                                                                                                                                 FXYD DOMAIN-CONTAINING ION TRANSPORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEVELOPMENTAL STAGE: HIGHEST LEVELS AT THE EMBRYONIC STAGE, DECREASING PROGRESSIVELY DURING DEVELOPMENT, EXCEPT FOR AN INCREASE AT THE L3 STAGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 6; DB 1; Length 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 466FBF1E05D861C5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                            fransmembrane; Signal; Ionic channel; Ion transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Cell division control protein 42 homolog (CDC42CE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         188 AA
                                                                           SIMILARITY: BELONGS TO THE FXYD FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGULATOR 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRO-RICH.
                                                                                                                                                                                                                                                                                                         MICHARDON MINISTRATES EN MATERIAL MATER TO PROBLES ATPIGL_PLM_MATER PROSITE; PS01310; FXYD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          yeast mutation.";
J. Biol. Chem. 268:13280-13285(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.2%; Sc.
100.0%; Pre
                                                                                                                                                                                                                                                                      EMBL; U72680; AAB51040.1; -.
EMBL; AK003068; BAB22545.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              134 P
19454 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                21
178
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166
178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22
146
167
167
188
178 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
es 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@lib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENZYME REGULATION: ALTERNATE BETWEEN AN INACTIVE FORM BOUND TO GDP AND AN ACTIVE FORM BOUND TO GTP. ACTIVATED BY A GUANINE WOCLEOTIDE-EXCHANGE FACTOR (GEF) AND INACTIVATED BY A GTPASE-ACTIVATIOR PROTEIN (GAP).

SIMILARITY: BELONGS TO THE SMALL GTPASE SUPERFAMILY. RAS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Meleagris gallopavo (Common turkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1- FUNCTION: RAS PROTEINS BIND GDP/GTP AND POSSESS INTRINSIC GTPASE
                                                                                                                                                                                                                                                                                                             GTP-binding; Lipoprotein; Cell cycle; Cell division; Prenylation. NP_BIND 7 14 GTP (BY SIMILARITY). NP_BIND 54 58 GTP (BY SIMILARITY). NP_BIND 112 115 GTP (BY SIMILARITY).
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MEDLINE-97080492; PubMed-8921837;
Chajut A., Gazit A., Yaniv A.;
"The turkey c-raplA proto-oncogene is expressed via two distinct
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GERANYL-GERANYL (BY SIMILARITY).
8733958968681299 CRC64;
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01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Transforming protein p21 (K-Ras) (Ki-Ras).
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0; Mismatches
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InterPro: IPR001378; GTPase_Rho.
InterPro: IPR001806; Ras_trnsfrmng.
InterPro: IPR005225; Small_GTP.
Pfam; PF00071; ras; 1.
                                                                                                   EMBL; L10078; AAA51433.1; -.
EMBL; U23452; AAK31543.1; ALT_INIT.
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SMART; SM00174; RHO; 1.
TIGRFAMS; TIGRE00231; small_GTP; 1.
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HSSP; P21181; 1AM4.
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P79800;
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NP_BIND
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Baga M., Norgren M., Normark S.; "Biogenesis of E. coli Pap pill: papH, a minor pilin subunit involved in cell anchoring and length modulation."; cell 49:241-251(1987).
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"Nucleotide sequence, regulation and functional analysis of the pape gene required for cell surface localization of Pap pili of uropathogenic Escherichia coli.";

Mol. Microbiol. 1:169-178(1987).

-!- FUNCTION: FIMBRIAE (ALSO CALLED PILI), POLAR FILAMENTS RADIATING FROM THE SURFACE OF THE BACTERIUM TO A LENGTH OF 0.5-1.5 MICROMETERS AND NUMBERING 100-300 PER CELL, ENABLE BACTERIA TO COLONIZE THE EPITHELLIUM OF SPECIFIC HOST ORGANS.

-!- FUNCTION: PAPH SEEMS TO ANCHOR THE PILUS TO THE BACTERIAL CELL. IN ADDITION THE STOLGHOMETRIC RELATIONSHIP BETWEEN PAPH AND PAPA DETERMINES THE PILUS LENGTH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-93023852; PubMed-1357526; Marklund B.-I., Tennent J.M., Garcia E., Hamers A., Baga M., Lindberg F., Gaastra W., Mormark S., "Horizontal gene transfer of the Escherichia coli pap and prs pill operons as a mechanism for the development of tissue-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
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Proto-oncogene; GTP-binding; Prenylation; Lipoprotein.
NP_BIND 10 17 GTP (BY SIMILARITY).
NP_BIND 57 61 GTP (BY SIMILARITY).
NP_BIND 116 119 GTP (BY SIMILARITY).
NP_BIND 116 119 GTP (BY SIMILARITY).
DOMAIN 32 40 EFFECTOR REGION (BY SIMILARITY).
LIPID 185 185 FARNESYL (BY SIMILARITY).
SEQUENCE 188 AA; 21452 MW; AAB6C319BB259865 CRC64;
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01-APR-1988 (Rel. 07, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
PAP fimbrial minor pilin protein precursor.
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100.0%; Pred. No.
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HSSP; P01112; 1PLL.
InterPro; IPR001377; GTPase_Ras.
InterPro; IPR001230; Prenyl_site.
InterPro; IPR001806; Ras_trnsfrmng.
InterPro; IPR005225; Small_GTP.
Pfam; PF00071; ras; 1.
PRIWYS; PR00449; RASTRNSFRMG.
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SEQUENCE OF 149-195 FROM N.A.
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P07111;
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; Sequence 1098, Application 
; Patent No. US20020055627A1
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; ORGANISM: Homo
US-09-764-869-926
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC007
                                                                                                                      PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 2442 SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 926
                                                Query Match
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CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR FILING DATE: 2000-03-08
                                                                                                                                                                                                                                                  APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/764,869
CURRENT FILING DATE: 2001-01-17
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TYPE: PRT
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OTHER INFORMATION: Xaa
NAME/KEY: SITE
LOCATION: (40)
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                       Score 6; DB 1; Pred. No. 27; 0; Mismatches
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CURRENT FILING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: EARLIER APPLICA
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               FILING DATE: EARLIER FILING APPLICATION NUMBER: EARLIER
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SEQ ID NO 1820
LENGTH: 36
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Patent No. US20020147140A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC005
                                                                              Query Match
Best Local
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CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM
NUMBER OF SEQ ID NOS: 4031
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TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PAIO1
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TYPE: PRT
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LOCATION: (1)
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LOCATION: (32)
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CURRENT FILLING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-03-08
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CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-03-08
                                                  NAME/KEY: SITE
LOCATION: (31)
OTHER INFORMATION: )
NAME/KEY: SITE
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TITLE OF INVENTION: Nucleic Acids, Proteins
FILE REFERENCE: PA106
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TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA106
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TYPE: PRT
OTHER INFORMATION:
NAME/KEY: SITE
                                                                                                                       ORGANISM: Homo sapiens FEATURE:
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OTHER INFORMATION:
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ORGANISM: Homo sapiens
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; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-925-299-1319
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Patent No.
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Best Local
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OTHER INFORMATION: Xaa
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                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
                                                                                                                                                                                                                                              NAME: Bastlan, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 02:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,838
FILING DATE: 01-MAY-1998
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TITLE OF INVENTION: Nucleic Acids That Control Seed and
TITLE OF INVENTION: Fruit Development in Plants
                                                                                                                                       MOLECULE TYPE:
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                             TFGKKK 53
TFGKKK 6
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5. US20020152501A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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Yadegari, Ramin
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                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Harada, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fischer, Robert L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                       peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xaa
                                                                         10.2%; Score 6; 100.0%; Pred. No.
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; OTHER INFORMATION: X
; NAME/KEY: SITE
; LOCATION: (31)
; OTHER INFORMATION: X
US-09-925-299-1474
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US-09-764-846-248
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LENGTH: 31
TYPE: PRT
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PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1474
LENGTH: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: ROSen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA102
                                                                            Query Match
Best Local Similarity
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                                                               Matches
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CURRENT APPLICATION NUMBER: US/09/764,846

CURRENT FILING DATE: 2001-01-17
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                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: SITE
LOCATION: (25)
OTHER INFORMATION: X
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CURRENT FILING DATE: 2001-08-10
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NAME/KEY: SITE
LOCATION: (31)
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TYPE: PRT
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LOCATION: (30)
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                             23 EKKKKK 28
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les 6; Conserv
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EKKKKK 22
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                                                             Conservative
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100.0%; Pred. No. 19
Live 0; Mismatches
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Pred. No.
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o. 19;
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APPLICANT: Hanzel, David K.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

FILE REFERENCE: ACCOMPACA - X - 1

CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT FILING DATE: 2001-05-23

PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR APPLICATION NUMBER: US 09/632,366

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR APPLICATION NUMBER: US 60/236,359
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Best Local Similarity 100.
George Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC007
CURRENT APPLICATION NUMBER: US/09/764,869
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                              APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K
APPLICANT: Chen, Wensheng
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TYPE: PRT
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les 6; Conserv
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APPLICATION NUMBER: PCT/US01/00666 FILING DATE: 2001-01-30
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Hanzel, David K.
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b; Pred. No. 11;
0; Mismatches
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PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/12
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1319
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US-09-925-299-1319
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Best Local
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LENGTH: 28
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (17)
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TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA102
CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
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OTHER INFORMATION:
OTHER INFORMATION:
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OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00662
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00661
OR APPLICATION NUMBER: PCT/US01/00670
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00670
OR APPLICATION NUMBER: US 60/234,687
OR APPLICATION NUMBER: US 60/234,687
OR FILING DATE: 2000-09-21
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00668
FILING DATE: 2001-01-30
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APPLICATION UMBER: PCT/US01/00664
FILING DATE: 2001-01-30
APPLICATION UMBER: PCT/US01/00669
FILING DATE: 2001-01-30
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N: EXPRESSED IN ADULT LIVER, SIGNAL = 5.7

N: EXPRESSED IN BARIN, SIGNAL = 2.7

N: EXPRESSED IN HONE MARROW, SIGNAL = 5.6

N: EXPRESSED IN LUNG, SIGNAL = 5.7

N: EXPRESSED IN HELA, SIGNAL = 3.6

N: EXPRESSED IN HEART, SIGNAL = 3.6

N: EXPRESSED IN HEART, SIGNAL = 4.8
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100.0%; Pr
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; Pred. No. 16
0; Mismatches
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US-09-945-249-87
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SEQ ID NO 87
LENGTH: 15
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PRIOR APPLICATION NUMBER: 09/041/990
PRIOR FILING DATE: 2001-01-13
PRIOR APPLICATION NUMBER: 08/771/212
PRIOR FILING DATE: 1996-12-20
PRIOR FILING DATE: 1996-12-20
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PRIOR FILING DATE: 1996-04-11
NUMBER OF SEQ ID NOS: 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION UMMBER: US/09/843,676
FILING DATE: 26-Apr-2001
CLASSIFICATION: 536
REFERENCE/DOCKET NUMBER: 015389-002930US TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 576-0200
                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 22 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Cech, Thomas R
                                                                                                                         APPLICATION NUMBER: US 08/846,017 FILING DATE: 25-APR-1997 APPLICATION NUMBER: US 08/844,419 FILING DATE: 18-APR-1997 APPLICATION NUMBER: US 08/724,643 FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: Two Embarcac
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: United States of America
                                                           NAME: Apple, Randolph T. REGISTRATION NUMBER: 36,429
                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/854,050 FILING DATE: 09-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
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INVENTION: No. US20020164786A1el Telomerase
F SEQUENCES: 225
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US-09-438-486-201
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APPLICATION NUMBER: US
FILING DATE: 06-MAY-15
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
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SEQUENCE CHARACTERISTICS:
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T
REGISTRATION NUMBER: 36,
                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 01
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 18-APR-
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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CORRESPONDENCE ADDRESS:
Townsend and Townsend and Crew LLP
ADDRESSEE: Two Embarcadero Center, 8th Floor
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                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/0 FILING DATE: 12-NOV-1999 CLASSIFICATION: 536
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                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/846,017 FILING DATE: 25-APR-1997
                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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mes 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94111-3834
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
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Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
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06-MAY-1997
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100.0%; Pr
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Pred. No.
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RESULT 4 US-09-764-877-1759 8 8

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EKKKKKT 29

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 155
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-774-639-155
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US-09-74-639-155
Sequence 155, Application US/09774639
Publication No. US2003000355A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 90 Human Secreted Proteins
FILE REFERENCE: PZ013P1
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US-10-014-717-5
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                                                                                                         Sequence 5, Application US/10014717 Publication No. US20020192778A1 GENERAL INFORMATION:
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC005
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Best Local s
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                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/244,112 PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-04 NUMBER OF SEQ ID NOS: 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/764,877
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 4031
                                       APPLICANT:
                                                                     APPLICANT: Schupp, Thomas APPLICANT: Ligon, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/774,639
CURRENT FILING DATE: 2001-07-09
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Cyr, Devon
Goerlach, Joern
                                                    Molnar, Istvan
                                   Zirkle, Ross
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100.0%; Pred. No.
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Pred. No.
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5. 6.7;
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; SEQ ID NO 5
; LENGTH: 7257
; TYPE: PRT
; ORGANISM: Sorangium cellulosum
US-10-014-717-5
                                                                                     Sequence 87, Application US/09945249
Patent NO. US20020168748A1
GENERAL INFORMATION:
APPLICANT: BERLIN, VIVIAN
APPLICANT: DAMAGNEZ, VERONIQUE
APPLICANT: SMITH, SUSAN E.
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CURRENT FILING DATE: 2001-10-23
PRIOR APPLICATION NUMBER: JP 294795/2001
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: JP 227094/2001
PRIOR FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: JP 6910/2001
PRIOR APPLICATION NUMBER: JP 6910/2001
PRIOR FILING DATE: 2001-01-15
PRIOR APPLICATION NUMBER: JP 401417/2000
PRIOR FILING DATE: 2000-12-28
PRIOR FILING DATE: 2000-12-28
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Best Local Similarity
Matches 6; Conserv
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
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               APPLICANT: DAMAGNEZ, VERONIQUE
APPLICANT: SMITH, SUSAN E.
TITLE OF INVENTION: ASSAYS AND REAGENTS FOR IDENTIFYING ANTI-FUNGAL AGENTS,
TITLE OF INVENTION: AND USES RELATED THERETO
FILE REFERENCE: MIV-074.06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US/09/335,409
PRIOR FILING DATE: 1399-06-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Process for Producing Peptides By Using In Vitro TITLE OF INVENTION: Transcription/Translation System FILE REFERENCE: 1752-0151P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES FILE REFERENCE: 4-30582A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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CURRENT FILING DATE: 2001-11-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 30
CURRENT APPLICATION NUMBER: US/09/945,249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 14
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                    23 EKKKKK 28
                                                                                                                                                                                                                                                                                                              9 EKKKKK 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SHIMIZU, YOShihiro
UEDA, Takuya
                                                                                                                                                                                                                                                                                                                                                                                              10.2%; Score 6; lilarity 100.0%; Pred. No. Conservative 0; Mismatcl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.9%; Score 7; DB ilarity 100.0%; Pred. No. 1. Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                       DB 10;
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5. 1.7e+02
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 14;
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Hanzel, David I Chen, Wensheng

David K.

FOR

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OTHER INFORMATION: EXPRESSED IN LUNG, S
OTHER INFORMATION: EXPRESSED IN ADULT IN
OTHER INFORMATION: EXPRESSED IN PLACENT
OTHER INFORMATION: EXPRESSED IN BRAIN,
OTHER INFORMATION: EXPRESSED IN BONE MA
OTHER INFORMATION: EXPRESSED IN FETAL IN
OTHER INFORMATION: EXPRESSED IN BT474,
OTHER INFORMATION: EXPRESSED IN HEART,
OTHER INFORMA
                                                                                                                                                                                                   Query Match
Best Local
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PRIOR EFILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
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PRIOR FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'ILE REFERENCE: Aeomica-X-1
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                                                 KVHGSLARAGKVRGQTPKVAKQEKKKKK 28
KVHGSLARAGKVRGQTPKVAKQEKKKKK 83
                                                                                                                                                                                                   Similarity
                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                    N. EXPRESSED IN PLACENTA, SIGNAL = 18

N. EXPRESSED IN BRAIN, SIGNAL = 5.5

N. EXPRESSED IN BONE MARROW, SIGNAL = 9.3

N. EXPRESSED IN FETAL LIVER, SIGNAL = 4.1

N. EXPRESSED IN HEAT, SIGNAL = 12

N. EXPRESSED IN HEAT, SIGNAL = 12

N. EXPRESSED IN HELA, SIGNAL = 12
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                                                                                                                                                                                           Score 28;
Pred. No.
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ADULT LIVER, SIGNAL
                                                                                                                                                         Mismatches
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2.8e-19;
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US-09-864-761-39484
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                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 39484
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                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo s
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence
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OTHER INFORMATION:
OTHER INFORMATION:
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OR APPLICATION NUMBER: PCT/US01/00669
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00665
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00668
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00663
OR FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00667
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00664
                                                                                                                                                           R INFORMATION: I
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APPLICATION NUMBER: US 60/234,687
FILING DATE: 2000-09-21
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APPLICATION NUMBER: PCT/US01/00662
FILING DATE: 2001-01-30
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                                                                                                    N: MAP TO ACO05598.6

N: EXPRESSED IN PADULT LIVER, SIGNAL = 7.1

N: EXPRESSED IN LUNG, SIGNAL = 7.4

N: EXPRESSED IN HELA, SIGNAL = 7.7

N: EXPRESSED IN HELA, SIGNAL = 7.7

N: EXPRESSED IN HEART, SIGNAL = 7.3

N: EXPRESSED IN BRAIN, SIGNAL = 6.
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2000-06-30
09/774,203
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                     11.9%;
Score 7; DB 1
3; Pred. No. 3.9
0; Mismatches
                     DB 10;
o. 3.9;
                                          Length 62
                                                                                                           6.7
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Matches

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Maximum DB
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47.5
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Match Length
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59
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       Published_Applications_AA: *
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: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
1: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US0_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KVHGSLARAGKVRGQTPKVA.....RRFVNVVPTFGKKKGPNANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GenCore version 5.1.3 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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       10 US-09-925-301-994

10 US-09-864-761-35333

10 US-09-864-761-35338

10 US-09-864-877-1759

10 US-09-774-639-155

10 US-09-983-067-1

10 US-09-983-067-1

10 US-09-984-676-201

10 US-09-844-676-201

10 US-09-864-761-41097

10 US-09-864-761-41097

10 US-09-925-299-1319

10 US-09-925-299-1319

10 US-09-925-299-1474

10 US-09-925-301-1640
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Sequence 5, Appli
Sequence 1, Appli
Sequence 87, Appl
Sequence 201, App
Sequence 201, App
Sequence 729, App
Sequence 1319, Ap
Sequence 189, App
Sequence 1474, Ap
Sequence 1474, Ap
Sequence 1043, Ap
Sequence 1043, Ap
Sequence 1640, Ap
                                                                                                                                                                                                                                                                                                        Description
                                                                                                                                                                                                                             Sequence 994, App
Sequence 35333, A
Sequence 39484, A
Sequence 1759, Ap
                                                                                                                                                                                Sequence 155, App
Sequence 5, Appli
Sequence 1, Appli
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| 4                 | 44                | 43                 | 42                | 41                 | 40                | 39               | 38               | 37                | 36                 | 35                | 34                  | ω<br>ω            | 32              | 31                 | 30                 | 29                | 28                  | 27                  | 26                | 25                | 24                 | 23                | 22                 | 21                | 20                 |
|-------------------|-------------------|--------------------|-------------------|--------------------|-------------------|------------------|------------------|-------------------|--------------------|-------------------|---------------------|-------------------|-----------------|--------------------|--------------------|-------------------|---------------------|---------------------|-------------------|-------------------|--------------------|-------------------|--------------------|-------------------|--------------------|
| σ                 | , 01              | 0                  | 6                 | σ                  | 6                 | 6                | 0                | 6                 | 6                  | σ                 | σ                   | 6                 | σ               | σ                  | 6                  | 6                 | 6                   | 6                   | 5                 | 6                 | σ                  | 0                 | 6                  | 6                 | 6                  |
| 7.07              | 10.2              | 10.2               | 10.2              | 10.2               | 10.2              | 10.2             | 10.2             | 10.2              | 10.2               | 10.2              | 10.2                | 10.2              | 10.2            | 10.2               | 10.2               | 10.2              | 10.2                | 10.2                | 10.2              | 10.2              | 10.2               | 10.2              |                    | 10.2              | 10.2               |
| 7                 | 73                | 72                 | 72                | 69                 | 89                | 83               | 83               | 67                | 66                 | 66                | 64                  | 63                | 63              | 62                 | 60                 | 60                | 59                  | 57                  | 56                | 55                | 52                 | 51                | 48                 | 45                | 43                 |
| TO                | 10                | 10                 | 10                | 10                 | 10                | 9                | 9                | 10                | 10                 | 10                | 10                  | 10                | 9               | 10                 | 10                 | 9                 | 10                  | 10                  | 10                | 10                | 10                 | 9                 | 10                 | 10                | 10                 |
| US-09-833-06/-9   | US-09-764-846-242 | US-09-925-300-1105 | US-09-764-846-179 | US-09-925-299-1340 | US-09-764-846-191 | US-09-201-936-19 | US-09-201-936-18 | US-09-867-550-284 | US-09-764-877-1089 | US-09-764-846-224 | US-09-864-761-45501 | US-09-764-846-260 | US-10-117-604-2 | US-09-925-301-1475 | US-09-925-300-1198 | US-09-989-919-118 | US-09-864-761-47812 | US-09-864-761-47593 | US-09-764-847-601 | US-09-764-855-113 | US-09-764-869-1228 | US-09-983-802-479 | US-09-925-299-1098 | US-09-764-869-926 | us-09-925-301-1633 |
| Sequence 9, Appli | 242,              | •                  | Sequence 179, App | Sequence 1340, Ap  | Sequence 191, App |                  | 18,              | Sequence 284, App | 10                 | Sequence 224, App | Sequence 45501, A   | Sequence 260, App | 2, App          | Sequence 1475, Ap  | Sequence 1198, Ap  | Sequence 118, App | Sequence 47812, A   | Sequence 47593, A   | Sequence 601, App | Sequence 113, App | Sequence 1228, Ap  | Sequence 479, App | Sequence 1098, Ap  |                   | Sequence 1633, Ap  |

## ALIGNMENTS

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: Sequence 35333, Application US/09864761
Patent No. US20020048763A1
: GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
: APPLICANT: Rank, David R.
                                                                                                    RESULT 2
US-09-864-761-35333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 1
US-09-925-301-994
; Sequence 994, Application US/09925301
; Patent No. US20020052308A1
                                                                                                                                                                                                                                                                                                                                                         US-09-925-301-994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA106
                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 994
LENGTH: 170
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
FEATURE:
NAME/KEY: SITE
LOCATION: (5)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                    Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 59; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/925,301 CURRENT FILING DATE: 2001-08-10
                                                                                                                                                                                     0
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Pred. No. 9.3e-48;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                 Length 170;
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RESULT 32
PRSH_ECAL
IDS PRSH_E
AC P42185
DT 01-NOV
DT 01-NOV
DT 15-DEC
DE PRSH.
GN PRSH.
OS Bacter
OC Escher
OC ESCHER
RN [1]
RP SEQUEN
RC STRAIN
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Best Local
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                                                                                                          adhesive properties.";

Mol. Microbiol. 6:2225-2242(1992).

Mol. Microbiol. 6:2225-2242(1992).

POLAR FILAMENTS RADIATING FUNCTION: FIMBRIAE (ALSO CALLED PILI), POLAR FILAMENTS RADIATING FROM THE SURFACE OF THE BACTERIUM TO A LENGTH OF 0.5-1.5

MICROMETERS AND NUMBERING 100-300 PER CELL, ENABLE BACTERIA TO COLONIZE THE EPITHELIUM OF SPECIFIC HOST ORGANS.

PONCTION: PRSH SEEMS TO ANCHOR THE PILUS TO THE BACTERIAL CELL. IN ADDITION THE STOICHLOMETRIC RELATIONSHIP BETWEEN PRSH AND PRSA DETERMINES THE PILUS LENGTH.

SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1995 (Rel.
01-NOV-1995 (Rel.
15-DEC-1998 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; Y00529; CAA68587.1; -. EMBL; M16202; AAA24286.1; -. EMBL; X61239; CAA43563.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                     Marklund B.-I., Tennent J.M., García E., Hamers A., Baga M.,
Lindberg F., Gaastra W., Normark S.;
"Horizontal gene transfer of the Escherichia coli pap and prs pili
operons as a mechanism for the development of tissue-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fimbria;
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  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-1442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRS fimbrial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; A27021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=93023852; PubMed=1357526;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Escherichia
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URINARY TRACT PRODUCE PAP-PILI WHICH RARE HAIT-LIKE APPENDAN
CONSISTING OF ABOUT 1000 HELICALLY ARRANGED SUBUNITS OF THE
PROTEIN PAPA. THESE PILI MEDIATE BINDING TO DIGALACTOSIDE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Secreted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONTAINING GLYCOLIPIDS PRESENT ON THE EPITHELIAL CELLS WHICH
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6; Conserv
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58
195
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. 32, Last sequ
. 37, Last anno
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37, Last annotation update)
pilin protein precursor.
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195
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21835 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gamma subdivision; Enterobacteriaceae;
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Pred. No. 48;
0; Mismatches
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Best Local
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P40993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
DISULFID
                                                                                                                                                                                                                                    Dietrich F.S., Mulligan J., Allen E., Araujo R., Aviles E.,
Berno A., Carpenter J., Chen E., Cherry J.M., Chung E., Duncan
Hunicke-Smith S., Hyman R., Komp C., Lashkari D., Lew H., Lin E
Mosedale D., Nakahara K., Namath A., Oefner P., Oh C., Petel F.
Roberts D., Schramm S., Schroeder M., Shogren T., Shroff N.,
Winant A., Yelton M., Botstein D., Davis R.W.;
Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
-!- FUNCTION: ESSENTIAL COMPONENT OF THE MRP RIBONUCLEOPROTEIN
ENDORIBONUCLEASE THAT CLEAVES MITOCHONDRIAL PRIMER RNA SEQU-
-!- SUBUNIT: HOMODIMER (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                             Schmitt M.E., Clayton D.A.; "Characterization of a unique protein component of yeast RNase MRP: an RNA-binding protein with a zinc-cluster domain."; Genes Dev. 8:2617-2628(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation updat
                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharomyces cerevisiae (Baker's yeast).

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X62157; CAA44082.1; -
SEQUENCE
                          SGD; S0002886; SNM1.
Hydrolase; Nuclease; RNA-binding.
                                                       EMBL; 237982; CAAB6054.1;
EMBL; U33050; AAB64905.1;
PIR; S48236; S48236.
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-95047399;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RNase MRP protein component SNM1.
SNM1'OR YDR478W OR D8035.21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fimbria; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00419; Fimbrial;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 ARAGKV 12
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                                                                                                                                                                                                                                                                                                                                                                                          FROM N.A.
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198 AA;
               136
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195
97
21837
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100.0%; Prr
22541 MW;
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%; Pred. No. 48;
0; Mismatches
            LYS/
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PRS FIMBRIAL MINOR PILIN PROTEIN.
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67C262585D3BEA3A CRC64;
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               /SER-RICH
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Query Match

10.28;

Score 6;

DB 1;

Length 198;

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RESULT 34
RASM_HUMAN
ID MALMAN
ID MALMAN
ID MALMAN
ID 30-MAY
DT 30
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Matches 6; Conserv
                                                                                                             SMART; SM00173; RATIGREAMS; TTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAY-2000
30-MAY-2000
15-JUN-2002
                       NP_BIND
                                                                                                                                                                                                 Genew: HGNC:7227; MRAS.
InterPro; IPR003577; GTPase_Ras.
InterPro; IPR001230; Prenyl_site.
InterPro; IPR001806; Ras_trnsfrmng.
InterPro; IPR005225; Small_GTP.
Pfam; PF00071; ras; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=98062166; PubMed=9400994; Kimmelnan A., Tolkacheva T., Lorenzi M.V., Osada M., Chan A.M.-L.; "Identification and characterization of R-ras3: a novel member of RAS gene family with a non-ubiquitous pattern of tissue distribution.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=99409042; PubMed=10477695;
Louahed J., Grasso L., de Smet C., van Roost E., v
Nicolaides N.C., Levitt R.C., Renauld J.-C.;
"Interleukin-9-induced expression of M-Ras/R-Ras3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the Swiss Institute of Bioinformatics and the EMBL outst
the European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                014807;
    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RASM_HUMAN
                                                                                        NP_BIND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 VVPTFG 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45 VVPTFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Od 94:1701-1710(1999).

FUNCTION: MAY SERVE AS AN IMPORTANT SIGNAL TRANSDUCER FOR UPSTREAM STIMULI IN CONTROLLING CELL PROLIFERATION. WEAK ACTIVATES THE MAP KINASE PATHWAY.

TISSUE SPECIFICITY: EXPRESSION HIGHLY RESTRICTED TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INDUCTION: BY INTERLEUKIN-9, BUT NOT SIMILARITY: TO RAS PROTEINS. BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HEART
                                                                                                                                                                                                                                                                                                                                                                   AF043938;
                                                                                                                                                                                                                                                                                                                                                                                     AF022080;
                                                                                                                                       00173; RAS;
TIGR00231;
                                                                                                                                                                                                                                                                                                                                                                                                                                  email to license@isb-sib.ch).
; Prenylation;
20 27
1 71
126 129
42 50
185 191
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(Rel. 39, Last sequence up
(Rel. 41, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50
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AAD02287.1;
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                                                                                                                                       small_GTP;
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POLY-LYS.
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Catarrhini; Hominidae;
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                                            (BY SIMILARITY).
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                       REGION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIGNAL TRANSDUCER FOR A NOVEL PROLIFERATION. WEAKLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY IL-2 OR IL-4.
TO THE R-RAS SUB-FAMILY.
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                       SIMILARITY).
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PRINTS; SMART; S

SM00173;

RAS;

RASTRNSFRMNG

TIGR00231;

small\_GTP;

InterPro; IPR005225;
Pfam; PF00071; ras;
PRINTS; PR00449; RAS

InterPro; InterPro;

IPR003577; GTPase\_Ras.
IPR001230; Prenyl\_site.

InterPro;

IPR001806;

Ras\_trnsfrmng

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RESULT TO COLUMN TO COLUMN
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Best Local
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microspikes R
MRAS OR XRAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Leslie K.B., Schrader J.W.;

Leslie K.B., Schrader J.W.;

"Characterization of a transforming, novel ras-related molecule.",

"Characterization of a transforming, novel ras-related molecule.",

"Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.

-i- FUNCTION: MAY SERVE AS AN IMPORTANY SIGNAL TRANSDUCER FOR A NO

UPSTREAM STIMULI IN CONTROLLING CELL PROLIFERATION. WEAKLY

ACTIVATES THE MAP KINASE PATHWAY (BY SIMILARITY).

-i- SIMILARITY: TO RAS PROTEINS. BELONGS TO THE R-RAS SUB-FAMILY.
                                                                                                                                                                                                                                                            EMBL; AB004879; BAA20538.1; -.
EMBL; AF043581; AAD02277.1; -.
EMBL; AF031159; AAD01926.1; -.
HSSP; P01112; 1PLK.
MGD; MGI:1100856; MGAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a content of the EWBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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SEQUENCE
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Louahed J., Grasso L., de Smet C., van Roost E.,
Nicolaides N.C., Levitt R.C., Renauld J.-C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
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Novel small GTPase M-Ras
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1. 40, Last annotation u
tein M-Ras (Ras-related
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RESULT 36
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SEQUENCE
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                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                        Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.

1. FUNCTION: MAY SERVE AS AN IMPORTANT SIGNAL TRANSDUCER FOR A NUPSTREAM STIMULI IN CONTROLLING CELL PROLIFERATION. MEAKLY ACTIVATES THE MAP KINASE PATHWAY (BY SIMILARITY).

1. TISSUE SPECIFICITY: EXPRESSED IN SKELETAL MUSCLE CELLS.

1. SIMILARITY: TO RAS PROTEINS. BELONGS TO THE R-RAS SUB-FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Métazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
                                                       TIGREAMS; TIC
GTP-binding;
                                                                                        PRINTS;
                                                                                                             InterPro; IPR003577; GTPase_Ras.
InterPro; IPR001230; Prenyl_site
InterPro; IPR001806; Ras_trnsfrm
InterPro; IPR005225; Small_GTP.
                                                                                                                                                           EMBL; D89863; BAA20531.1; HSSP; P01112; 1PLK.
                                                                                                                                                                                                                                                                                                                                                                                                     cytoskeleton
                                                                                                                                                                                                                                                                                                                                                                                                       Matsumoto K., Asano T., Endo T.;
"Novel small GTPase M-Ras participates
cytoskeleton.":
                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=98055615; PubMed=9395237;
Matsumoto K., Asano T., Endo T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
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                                                                                                    Pfam; PF00071; ras;
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                                                               SM00173; RAS;
MS; TIGR00231;
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g; Prenylation;
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Small_GTP.
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EFFECTOR REGION (
POLY-LYS.
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; Lipoprotein.
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
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Pred. No
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: 975CFDD1FDF37FCF CRC64;
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RESULT 37
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AC P57212
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OS Symbio
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Nature 407:81-86(2000).

CHATALYZING THE FORMATION OF RIBOFLAVIN FROM 5-AMINO-6-(1'-D)-C CATALYZING THE FORMATION OF RIBOFLAVIN FROM 5-AMINO-6-(1'-D)-C C RIBITYL-AMINO-2,4(1H,3H)-PYRIMIDINED NOB AND L-3,4-DIHYDROHY-2-BUTANONE-4-PHOSPHATE VIA 6,7-DIMETHYL-8-LUMAZINE. THE ALPHA SUBUNIT CATALYZES THE DISMUTATION OF 6,7-DIMETHYL-8-LUMAZINE TO C RIBOFLAVIN AND 5-AMINO-6-(1'-D)-RIBITYL-AMINO-2,4(1H,3H)-C PYRIMIDINEDIONE (BY SIMILARITY)-8-(1-D-ribityl)lumazine riboflavin + 4-(1-D-ribitylamino)-5-amino-2,6-dihydroxypyrimidine.

C-I-SUBUNITS (BY SIMILARITY).

C-I-SUBUNITS (BY SIMILARITY).

C-I-SUBUNITS (BY SIMILARITY).
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Best Local 9
      Query Match
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial antitues requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibj.ghp.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-Tokyo 1998;
MEDLINE-20445173; PubMed-10993077;
Shigenobu S., Watanabe H., Hattori M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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REPEAT
                                                                                                                                                                                    EMBL; AP001118; BAB12830.1; --
InterPro; IPR001783; Lum_binding.
Pfam; PF00677; Lum_binding; 2.
ProDom; PD004110; Lum_binding; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             symbiotic bacterium).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Buchnera aphidicola
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RISA_BUCAI
                                                                                                                         Riboflavin biosynthesis; Transferase; REPEAT 1 97 1.
                                                                                                                                                      TIGRFAMS; TIGR00187; ribE; 1. PROSITE; PS00693; LUM_BINDING;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=118099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity hes 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24 KKKKKT
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                                                                       201
85
183
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100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23887 MW;
                                                         23505
      10.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           H., Hattori M., Sakaki Y., Ishikawa
endocellular bacterial symbiont of
                                                         MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gamma subdivision; Buchnera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 6; DB 1; Pred. No. 51; 0; Mismatches
      Score 6; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GERANYL-GERANYL (BY SIMILARITY).; 0869627A12C67EBA CRC64;
                                                     BINDS TO LUMAZINE (PROBABLE).
BINDS TO LUMAZINE (PROBABLE).
; 7CCE3272CF54BA5B CRC64;
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DB
51;
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                                                                                                                                     Complete proteome.
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                    Length 208
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aphids
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Matches

Similarity
6; Conserv

Conservative

0

Mismatches

0

Indels

0

Gaps

В Ş

16

21 28

23

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RESULT 38

RHO1_YEAST
ID RHO1_Y
AC P06780
DT 01-JUN
DT 0
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01-JAN-1988
01-JAN-1988
                                                                                                                                                                                                 EMBL; M15189; AAA34977.1; -.
EMBL; U25840; AAB68152.1; -.
EMBL; M15161; AAA74729.1; -.
PIR; A26587; TVBYH1.
                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Myers A.M., Crivellone M.D., Tzagoloff A.;
"Assembly of the mitochondrial membrane system. MRP1 and MRP2, two
yeast nuclear genes coding for mitochondrial ribosomal proteins.";
J. Biol. Chem. 262:3388-3397(1987).
-!- SIMILARITY: BELONGS TO THE SMALL GTPASE SUPERFAMILY. RHO FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN-$288c / AB972; MEDLINE-97313271; PubMed-9169875;
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 201-209 FROM N.A. MEDLINE-87137621; PubMed-3029111;
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"Characterization of two members of the rho gene yeast Saccharomyces cerevisiae.";
Proc. Natl. Acad. Sci. U.S.A. 84:779-783(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RHO1 protein.
RHO1 OR YPR165W OR P9325.3.
                                                                                                                   HSSP; P06749; 1FTN.
SGD; S0006369; RHO1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 387:103-105(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE-87118248; PubMed-3543936;
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InterPro;
                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The nucleotide sequence of Saccharomyces cerevisiae chromosome XVI.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUN-2002
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EKKKKK
                                     IPR003578; GTPase_Rho.
IPR001230; Prenyl_site
IPR001806;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Rel. 06, Created)
(Rel. 06, Last sequence update)
(Rel. 41, Last annotation updat
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Ras_trnsfrmng
                                     Prenyl_site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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RESULT 40
KS1\_HYDAT
ID KS1\_H
AC P3897

KS1\_HYDAT P38978;

STANDARD;

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RESULT 39
T402_BURCE
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T402_BURCE STANDARD; PRT; 211 AA. P24536; 01-MAR-1992 (Rel. 21, Created) 01-MAR-1992 (Rel. 21, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update)
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                                                                                                       PIR; JQ1133; JQ1133.
InterPro; IPR002559; Transposase_11.
Pfam; PF01609; Transposase_11; 1.
Hypothetical protein; Transposable element; Transposition; DNA-binding; DNA recombination.
SEQUENCE 211 AA; 23968 MW; A5DC9E6961EA820B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Putative transposase for insertion sequence element IS402. Burkholderia cepacia (Pseudomonas cepacia). Bacteria; Proteobacteria; beta subdivision; Burkholderia group; Burkholderia.
                                                                                                                                                                                                                                                                                                                       -i- FUNCTION: INVOLVED IN THE TRANSPOSITION OF THE IN
SEQUENCE (By similarity).
-i- SIMILARITY: BELONGS TO THE TRANSPOSASE FAMILY 13.
                                                                                                                                                                                                                                                                                                                                                                 "Nucleotide sequence of IS402 from Pseudomonas cepacia."; Gene 102:143-144(1991).
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE=91323723; PubMed=1650732;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PRO0449; RASTRNSFRMNG.
SMART; SM00174; RHO; 1.
                                                                                                                                                                                      EMBL; M64065; -; NOT_ANNOTATED_CDS.
                                                                                                                                                                                                                                                                                                                                                                                           Ferrante A.A., Lessie
                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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 21
                                                                 Local Similarity
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                           4 GSLARA
GSLARA
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209 .
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122
39
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23152 MW;
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                                                                 100.0%;
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Pred. No.
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; 630B17E9E34CFE75 CRC64;
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GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
EFFECTOR REGION (BY SIMILARITY).
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RESULT 41
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ID FLIZ_BA
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DT 01-JUN
DT 15-JUN
DT 15-JUN
DT FLIZ_C
GN FLIZ C
GN FLIZ C
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01-JUN-1994 (Rel.
15-JUN-2002 (Rel.
                                                                                                                                                                                                                                                                                                                                                        FLIZ_BACSU
P35536;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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KS1.
STRAIN=168 / OI1085;
MEDLINE=92283757; Pu
                                                                                                                                               Bacillus subtilis.
Bacteria; Firmicutes;
                                                                                                                                                                                                            Flagellar biosynthetic FLIZ OR CHEA.
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NCBI_TaxID=6087;
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c protein fliz precursor
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ASP/GLU-RICH (ACIDIC).
ARG/LYS-RICH (BASIC).
ASP/GLU-RICH (BASIC).
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POTENTIAL.
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50 AA APPROXIMATE REPEATS.
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responds to early signals of
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RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter M.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Fabret C., Ferrari E., Foulger D.,
RA Choi S.K., Codani J.J., Fabret C., Ferrari E., Foulger D.,
RA Choi S.K., Codani J.J., Fabret C., Ferrari E., Foulger D.,
RA Choi S.K., Codani J.J., Fabret C., Ferrari E., Foulger D.,
RA Choi S.K., Codani J.J., Fabret C., Ferrari E., Foulger D.,
RA Choi S.K., Codani J.J., Fabret C., Ferrari E., Foulger D.,
RA Choi S.K., Codani J.J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujlta M., Fujlta Y., Fuma S., Gallaron N.,
RA Fritz C., Fujlta M., Fujlta Y., Fuma S., Gallaron N.,
RA Fritz C., Fujlta M., Fujlta Y., Fuma S., Galleron N.,
RA Hilbert H., Halsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Guiseppi G., Guy B.J., Haga K., Haich J., Harwood C.R., Klein C.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Moone D., O'Reilly M., Ogawa K., Oylwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Roymolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sekiguchi J., Sekowska A., Serror S.J., Serror P., Shin B.S., Soldo B.,
RA Sekiguchi A., Tanakoshi A., Tanaka T., Texpstra P., Tognoni A.,
RA Viters P., Willet R., Wedler E., Wedler F., Vassmotti A.,
RA Viters P., Willet R., Vanameto H., Yata K.,
Yata M., Yata M., Yata M., Yata K.,
Yata M., Yata M., Yata M., Yata K.,
RA Yata M., Yata M., Ya
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Best Local
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M87005; AAA22452.1;
EMBL; Z99112; CAB13507.1;
PIR; B41886; B41886.
SubtiList; BG10259; fliz.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 390:249-256(1997).
-!- FUNCTION: MAY BE A STRUCTURAL COMPONENT OF THE FLAGELLUM THAT ANCHORS THE ROD TO THE MEMBRANE.
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bischoff D.S., Weinreich M.D., Ordal G.W.; "Nucleotide sequences of Bacillus subtilis flagellar biosynthetic genes flip and fliQ and identification of a novel flagellar gene, fliz.";
                                                                                                                                                                                                                                                                                                                                                                               SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                   Flagella;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The complete genome subtilis.";
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210 GKKKGP 215
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                                                                   GKKKGP 55
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                                                                                                                                       Similarity 6; Conserv
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Mismatches
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RESULT 42

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RESULT 43
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16-OCT-2001
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"Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. APS.";
Nature 407:81-86(2000).
-I- FUNCTION: EXCISES URACIL RESIDUES FROM THE DNA WHICH CAN ARIS AS A RESULT OF MISINCORPORATION OF DUMP RESIDUES BY DNA POLYMERASE OR DUE TO. DEAMILMATION OF CYTOSINE (BY SIMILARITY).
-I- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-I- SUBCELLULAR LOCATION: THE URACIL-DNA GLYCOSYLASE FAMILY.
                                                                                                                                                                                                                                                                          15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
30S ribosomal protein SJAe.
                                                                                                                                                                                                                                                                                                                                                                                      RS3A_PYRAE
Q8ZT21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro: IPR002043; U_DNA_g1ycSylse.
InterPro: IPR002243; U_DNA_g1ycSylse.
InterPro: IPR002249; U_g1ycosyl.
Pfam: PF03167; UDG; 1.
ProDom: PD001589; U_g1ycosyl; 1.
PROSITE: PS00130; U_DNA_GLYCOSYLASE; 1.
PROSITE: PS00130; U_DNA_GLYCOSYLASE; 1.
DNA repair; Hydrolase; Glycosidase; Complete proteome.
ACT_SITE
61
61
GENERAL BASE (BY SIMILARITY).
SEQUENCE 220 AA; 25653 MW; AEAF19BEE0A2942C CRC64;
                                                    SEQUENCE FROM N.A.
STRAIN-IM2 / ATCC 51768 / DSM 7523;
                                                                                                                                     Archaea; Crenarchaeota; Thermoprotei; Thermoproteales; Thermoproteaceae; Pyrobaculum.
NCBI_TaxID=13773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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P57280;
        Fitz-Gibbon
                                    PubMed=11792869;
                                                                                                                                                                                                                        Pyrobaculum aerophilum.
                                                                                                                                                                                                                                                   RPS3AE OR PAE3472
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(Rel. 40, Last sequence update)
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~1vcosylase (EC 3.2.2.-) (UDG).
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     Ladner H., Kim U.-J., Stetter K.O.,
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01-FEB-1996 (Rel. 33, I
01-OCT-1996 (Rel. 34, I
Hypothetical 26.9 kDa p
YJL148W OR J0637.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Katsoulou C., Tzermia M., Tavernarakis N., Alexandraki D.; "Sequence analysis of a 40.7 kb segment from the left arm of yeast chromosome X reveals 14 known genes and 13 new open reading frames including homologues of genes clustered on the right arm of chromosome XI.";
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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InterPro; IPR001593; Ribosomal_S3AE.
Pfam; PF01015; Ribosomal_S3AE; 1.
ProDom; PD003035; Ribosomal_S3AE; FALSE_NEG
PROSITE; PS01191; RIBOSOMAL_S3AE; FALSE_NEG
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                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ribosomal protein; Complete proteome. SEQUENCE 221 AA; 24761 MW; 19F917
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                                                                                                                                                                   Hypothetical
                                                                                                                                                                                                                         EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yeast 12:787-797(1996).
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MEDLINE=96408771; PubMed=8813765;
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X87371; CAA60807.1;
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DCD42DFEC574EDB6 CRC64;
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INO1-IDS2 intergenic region
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01-NOV-1997 (
01-NOV-1997 (
15-JUL-1998 (
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                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-Bristol N2;
MEDLINE-97153022; PubMed-8999956;
Tang Z., Okamoto T., Boontrakulpoontawee P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAV-1 OR T13F2.8.
Caenorhabditis elegans.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Identification, sequence, and expression of an invertebrate caveolin gene family from the nematode Caenorhabditis elegans. Implications for the molecular evolution of mammalian caveolin genes.";
J. Biol. Chem. 272:2437-2445(1997).
                                                                                          SEQUENCE
                                                                                                                                                          InterPro; IPR001612; Caveolin.
Pfam; PF01146; Caveolin; 1.
PROSITE; PS01210; CAVEOLIN; FALSE_NEG.
                                                                                                                                                                                               EMBL; Z81122; CAB03359.1; -. WormPep; T13F2.8; CE13633.
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TFGKKK 51
                                           6; Conserv
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183
234
235 /
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(Rel. 35, Last sequence update)
(Rel. 36, Last annotation update)
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ilarity 100.0%;
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235 C
234 P
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POTENTIAL.
CYTOPLASMIC (POTENTIAL).
PALMITATE (POTENTIAL).
F07B12DEB4D6F13A CRC64;
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                                           Score 6; DB 1;
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Search completed: February 6, 2003, 21:31:12 Job time: 14 secs

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RESULT 25
US-09-764-855-113
Sequence 113, Application US/09764855
Patent NO. US20020119919A1
GENERAL INFORMATION:
APPLICANT: ROSEN et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PA110
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US-09-764-869-1228
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Best Local Similarity
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                                                                                SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 113
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Matches 6; Conserv
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SEQ ID NO 479
LENGTH: 51
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CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/764,855 CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PC007
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                                                                                                                           Prior application data removed - NUMBER OF SEQ ID NOS: 334
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             LENGTH: 55
TYPE: PRT
ORGANISM: Homo sapiens
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FEATURE:
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0; Mismatches
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28;
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and
FILE REFERENCE: PC009
CURRENT APPLICATION NUMBER: US/09/764,847
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or
NUMBER OF SEQ ID NOS: 2003
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 601
LENGTH: 56
TYPE: PRT
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Best Local S
Matches 6
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Best Local S
Matches 6
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APPLICANT:
                                                                                                 PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
                                                                                                                                                                                                            TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY FILE REFERENCE: Accomica x-1 CURRENT APPLICATION NUMBER: US/09/864,761 CURRENT FILING DATE: 2001-05-23 PRIOR APPLICATION NUMBER: US 60/180,312 PRIOR APPLICATION NUMBER: US 60/180,312 PRIOR FILING DATE: 2000-02-04
         PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
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OTHER INFORMATION:
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Similarity 100.0%
6; Conservative
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Similarity 100.0%,
6; Conservative
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Hanzel, David K.
Chen, Wensheng
2001-01-30
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b; Pred. No. 30;
0; Mismatches
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Pred. No.
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GORGANISM: Homo sapiens
FEATURE:
FEATURE:
OTHER INFORMATION: MAP TO AL049694.9

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.85
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN PLACEWYA, SIGNAL = 0.9
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.80
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 0.88
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.80
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.80
OTHER INFORMATION: SWISSPROT HIT: BF344101.1, EVALUE 8.00e-14
US-09-864-761-47593
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Best Local Similarity
"heches 6; Conserve
                                                                     CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: GB 24263.6
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APPLICANT: Penn, Sharron G.
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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 47593
LENGTH: 57
                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
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PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
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APPLICATION NUMBER: PCT/US01/00665
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00668
FILING DATE: 2001-01-30
                       APPLICATION NUMBER: US 60/236,359 FILING DATE: 2000-09-27
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APPLICATION
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; OTHER INFORMATION: MAP TO AC010290.4
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.5
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.5
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.64
; OTHER INFORMATION: EST_HUMAN HIT: BE244981.1, EVALUE 1.00e-12
US-09-864-761-47812
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-989-919-118
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US-09-989-919-118
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PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOPTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 47812
                                                                                       NUMBER OF SEQ ID NOS: 124
SOFTWARE: PatentIn version
SEQ ID NO 118
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Best Local :
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APPLICANT: Macina, Retree
APPLICANT: Pluta, Jason
APPLICANT: Ghosh, Malavika
APPLICANT: Ghosh, Malavika
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Colon Specific Genes
FILE REFERENCE: DEX-0289
CURRENT APPLICATION NUMBER: US/09/989,919
CURRENT APPLICATION NUMBER: 05/252,505
PRIOR APPLICATION NUMBER: 60/252,505
PRIOR APPLICATION NUMBER: 60/252,505
PRIOR FILING DATE: 2000-11-21
PRIOR FILING DATE: 2000-11-22
NUMBER OF SEO IN NOS- 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. US20020164344A1
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16 EKKKKK 21
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nes 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/US01/00670 FILING DATE: 2001-01-30 APPLICATION NUMBER: US 60/234,687 FILING DATE: 2000-09-21
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APPLICATION NUMBER: PCT/US01/00661
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00668
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00663
APPLICATION NUMBER: PCT/US01/00663
FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00667
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00664
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 09/608,408 FILING DATE: 2000-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/US01/00662
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/09989919
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5. 32;
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and

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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins
FILE REFERENCE: PA106
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1594
SOFTWARE: Petentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 31
US-09-925-301-1475
Sequence 1475, Application US/09925301
; Patent No. US2002005230BA1
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; Sequence 1198, Application

; Patent No. US20020151681A1
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PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
SOFTWARE: PATENTIN VEr. 2.0
SEQ ID NO 1198
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                                                                                                                                                                                                                            SEQ ID NO 1475
LENGTH: 62
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Best Local Similarity
LOCATION: (8)
OTHER INFORMATION: X
NAME/KEY: SITE
'~~ATION: (9)
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Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Steve Ruben
TITLE OF INVENTION: Nucleic Acids, Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: PA101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Craig Rosen, APPLICANT: Steve Ruben
                                                                                    NAME/KEY: SITE
LOCATION: (5)
OTHER INFORMATION:
                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
                                                                                                                                 NAME/KEY: SITE LOCATION: (3)
OTHER INFORMATION:
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                                                                                                                                    Xaa
                                                                                    Xaa
                                        Xaa equals any of the naturally occurring L-amino acids
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Pred. No
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                                                                                    any of
                                                                                                                             any of the naturally occurring L-amino
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                                                                                    the naturally occurring
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32;
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b. 32;
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                                                                                    L-amino
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US-10-117-604-2
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      Matches
                  Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino NAME/KEY: SITE LOCATION: (48)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: SITE LOCATION: (60)
                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS_MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/10/117,604
FILING DATE: 04-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION NUMBER: US/08/971,089
FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL & FLORES, LLP
STREET: 4370 La Jolla Village Drive,
                                                                            TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: (
                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)535-9001
                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 60/030,987 FILING DATE: 15-NOV-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 63 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: NUCLEIC ACID ENCODING
SCHWANNOMIN-BINDING-PROTEINS AND PRODUCTS RELATED THERET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Pulst, Stefan M.
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6; Conserv
                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: California
COUNTRY: United States
                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                              NAME: Ramos, Robert T
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: San Diego
                                                                                                                                                                                   TELEFAX: (619)535-8949
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                                                                               SEQ
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Pred. No
                    Score 6;
Pred. No.
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                                                                               ID NO:
      Mismatches
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33;
                    DB 9;
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      Indels
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23 EKKKKK 28

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US-09-764-846-260

; Sequence 260, Application US/09764846

; Patent No. US20020102638A1
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Best Local Similarity
Watches 6; Conserve
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US-09-764-846-260
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APPLICATE: ROSEN et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PTI212

CURRENT APPLICATION NUMBER: US/09/764,846

CURRENT FILING DATE: 2001-01-17

Prior application data removed - consult PALM or file wrapper

NUMBER OF SEQ ID NOS: 348

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 260

LENGTH: 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -09-864-761-45501
                                                                                                                                                                                         PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
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TYPE: PRT
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                  APPLICATION NUMBER: PCT/US01/00665 FILING DATE: 2001-01-30 APPLICATION NUMBER: PCT/US01/00668 FILING DATE: 2001-01-30 APPLICATION NUMBER: PCT/US01/00663 FILING DATE: 2001-01-30
                                                                                                                                                                         FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00662
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RESULT 36
US-09-764-877-1089
; Sequence 1089, Application US/09764877
; Patent No. US20020147140A1
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Best Local S
Matches 6
                                                                   GENERAL INFORMATION:
APPLICANT: ROSEN et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PC005
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 224
LENGTH: 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 224, Application Patent No. US20020102638A1 GENERAL INFORMATION:
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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 45501
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                                 CURRENT APPLICATION NUMBER: US/09/764,877 CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/764,846 CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Prior application data removed - consult PALM NUMBER OF SEQ ID NOS: 348
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PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
Prior application data removed - refer to NUMBER OF SEQ ID NOS: 4031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: MAP TO AC008739.5
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.56
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.58
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.78
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.69
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.77
                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
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TYPE: PRT
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les 6; Conserv
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100.0%; Pr
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Pred. No.
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                PALM or file wrapper
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CURRENT APPLICATION NUMBER: US/09/201,936
CURRENT FILING DATE: 1998-12-01
EARLIER APPLICATION NUMBER: 09/011,356
EARLIER FILING DATE: 1998-02-04
EARLIER APPLICATION NUMBER: PCT/IB96/01022
EARLIER APPLICATION NUMBER: PCT/IB96/01022
EARLIER FILING DATE: 1996-08-05
EARLIER FILING DATE: 1995-08-05
EARLIER FILING DATE: 1995-12-22
EARLIER APPLICATION NUMBER: 08/511,485
EARLIER APPLICATION NUMBER: 08/511,485
EARLIER FILING DATE: 1995-08-04
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Best Local Similarity
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                                                                                                                                                                                              Sequence 18, Application US/09201936
Publication No. US20020187946A1
GENERAL INFORMATION:
APPLICANT: KORDELUK, Robert G.
APPLICANT: MacKenzie, Alexander E.
APPLICANT: Baird, Stephen
APPLICANT: Liston, Peter
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
FILE REFERENCE: 07891_003003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 2125
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 284
LENGTH: 67
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Mehraban, Fuad,
APPLICANT: Conley, Pamela
APPLICANT: Law, Debbie
APPLICANT: Topper, James
TITLE OF INVENTION: No. US20020082206A1el Polynucleotides from Atherogenic Cells and
TITLE OF INVENTION: Thereby 21402-013 (Cura-313)
FILE REFERENCE: 21402-013 (Cura-313)
CURRENT APPLICATION NUMBER: US/09/867,550
CURRENT FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: USN 60/208,427
PRIOR FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 2125
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Pred. No. 35;
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RESULT 40

US-09-764-846-191

(Sequence 191, Application US/09764846

Patent No. US20020102638A1

(GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PTZ12

CURRENT APPLICATION NUMBER: US/09/764,846

(CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIME!
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
FILE REFERENCE: 07891/003003
CURRENT APPLICATION NUMBER: US/09/201,936
CURRENT FILING DATE: 1998-12-01
EARLIER APPLICATION NUMBER: 09/011,356
EARLIER APPLICATION NUMBER: PCT/IB96/01022
EARLIER FILING DATE: 1998-02-04
EARLIER APPLICATION NUMBER: PCT/IB96/01022
EARLIER APPLICATION NUMBER: 08/576,956
EARLIER FILING DATE: 1995-08-05
EARLIER FILING DATE: 1995-08-04
EARLIER FILING DATE: 1995-08-04
EARLIER FILING DATE: 1995-08-04
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Best Local Similarity
"-+-hes 6; Conserv
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Best Local S
Matches 6
                                                    Prior application data removed - consult PALM NUMBER OF SEQ ID NOS: 348
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 191
LENGTH: 68
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 19
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APPLICANT: MacKenzie, Alexande
APPLICANT: Baird, Stephen
APPLICANT: Liston, Peter
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TYPE: PRT
ORGANISM: Homo sapiens FEATURE:
                                      TYPE: PRT
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les 6; Conserv
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100.0%; Pred. No. 35
Live 0; Mismatches
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); Pred. No. 35;
0; Mismatches
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o. 35;
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CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 1340
                                                                                                          RESULT 42
US-09-764-846-179
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; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (67)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-846-191
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Sequence 1340, Application US/09925299
Patent No. US20020055627A1
GENERAL INFORMATION:
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                                                                           Sequence 179, Application US/09764846 Patent No. US20020102638A1
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                                                             GENERAL INFORMATION:
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                APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ12
CURRENT APPLICATION NUMBER: US/09/764,846
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OTHER INFORMATION:
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; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 179

; LENGTH: 72

; TYPE: PRT

; ORGANISM: Homo sapiens

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US-09-764-846-242
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SEQ ID NO 1105
LENGTH: 72
TYPE: PRT
ORGANISM: Homo sapiens
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Matches 6
                                                                                            GENERAL INFORMATION:
APPLICANT: Rosen et al.
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                                                                                                                         Sequence 242, Application US/09764846 Patent No. US20020102638A1
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CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR FILING DATE: 2000-03-08
Prior application data removed - NUMBER OF SEQ ID NOS: 348
                              CURRENT APPLICATION NUMBER: US/09/764,846 CURRENT FILING DATE: 2001-01-17
                                                            TITLE OF INVENTION: Nucleic Acids, Proteins, FILE REFERENCE: PTZ12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/124,270 PRIOR FILING DATE: 1999-03-12 NUMBER OF SEQ ID NOS: 1890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Craig Rosen,
APPLICANT: Steve Ruben
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
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LOCATION: (65)
OTHER INFORMATION: Xaa
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SOFTWARE: PatentIn Ver. SEQ ID NO 242 LENGTH: 73

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RESULT 45
US-09-833-067-9
iSequence 9, Application US/09833067
Sequence 9, Application US/09833067
iSequence 9, Application US/09833067
iSequence 9, Application US2002054888A1
iSequence 9, Application US2002054888A1
iSequence 9, Application US2002048
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; ORGANISM: Homo sapiens
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Search completed: February 6, 2003, 21:32:50 Job time : 12 secs
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| 45                | 44                 | 43                 | 42                | 41                | 40                | 39                | 38                 | 37                | 36                | 35                | 34                | 33                | 32                 | 31                | 30                |
|-------------------|--------------------|--------------------|-------------------|-------------------|-------------------|-------------------|--------------------|-------------------|-------------------|-------------------|-------------------|-------------------|--------------------|-------------------|-------------------|
| 6                 | 6                  | 0                  | σ                 | 5                 | σ                 | 6                 | σ                  | 6                 | σ                 | 6                 | 6                 | 6                 | 6                  | σ                 | 6                 |
| 10.2              | 10.2               | 10.2               | 10.2              | 10.2              | 10.2              | 10.2              | 10.2               | 10.2              | 10.2              | 10.2              | 10.2              | 10.2              | 10.2               | 10.2              | 10.2              |
| 125               | 123                | 117                | 115               | 106               | 105               | 105               | 104                | 102               | 98                | 92                | 92                | 81                | 80                 | 74                | 70                |
| _                 | N                  | N                  | N                 | N                 | N                 | N                 | N                  | N                 | N                 | N                 | N                 | N                 | N                  | N                 | N                 |
| R3RT25            | B71268             | H84651             | S69849            | S59536            | PW0018            | PW0017            | C87604             | T07078            | н96585            | н82867            | T36134            | S66013            | B82267             | T47434            | Н97135            |
| ribosomal protein | probable ribosomal | hypothetical prote | hypothetical prot | cold stress prote | hypothetical prot | hypothetical prot | virulence-associat | cold stress prote | hypothetical prot | transcription reg | hypothetical prot | ribosomal protein | exodeoxyr1bonuclea | hypothetical prot | uncharacterized p |

## ALIGNMENTS

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probable ABC-type replicative DNA he Atu related protei hypothetical protee structural polypro hypothetical prote hypothetical prote hypothetical prote
C;Species: Homo Sapiens (Man)
C;Date: 30-Sep:1993 #sequence_revision 30-Sep-1993 #text_change 24-Sep-1999
C;Accession: JC1278; I37387; S68911; S21449; S21450
C;Accession: JC1278; L; Merregaert, J.
Blochem. Biophys. Res. Commun. 187, 927-933, 1992
A;Title: Genomic structure and expression of the human fau gene: Encoding the ribo A;Reference number: JC1278; MUID:92412144; PMID:1326960
A;Accession: JC1278
A;Molecule type: DNA
A;Residues: 1-133 <KAS>
A;Cross-references: EMBL:X65921; NID:931304; PIDN:CAN46714.1; PID:931305
A;Cross-references: EMBL:X65921; NID:931304; PIDN:CAN46714.1; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A.Cross-references: EMBL:X62671; NID:g407165; PIDN:CAA44545.1; PID:g57566
A;Accession: B47416
A;Accession: B47416
A;Molecule type: protein
A;Mesidues: 75-92 <OL2>
A;Note: the proteins are designated as ubiquitin-like protein and ribosomal protein 5;Superfamily: ubiquitin-like protein / rat ribosomal protein 530; ubiquitin homology
C;Superfamily: ubiquitin-like protein / rat ribosomal protein 530; ubiquitin homology
F;1-74/Product: ubiquitin-like protein #status predicted <UBI>
F;1-74/Pomain: ubiquitin homology <UBH>
F;75-133/Product: ribosomal protein 530 #status experimental <RIB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ubiquitin-like protein / ribosomal protein S30, cytosolic [validated] - rat N;Contains: ribosomal protein S30; ubiquitin-like protein C;Species: Rattus norvegicus (Norway rat) C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 21-Jul-2000 C;Accession: A47416; B47416; S18101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Olvera, J.; Wool, I.G.
J. Biol. Chem. 268, 17967-17974, 1993
A;Title: The carboxyl extension of a ubiquitin-like protein is A;Reference number: A47416; MUID:93352612; PMID:8394356
A;Accession: A47416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
JC1278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ubiquitin-like protein / ribosomal protein S30, N;Alternate names: fau protein
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A; Residues: 1-133 <OLV>
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Pred. No. 5.2e-52;
; Mismatches 0;
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A.Status: preliminary
A.Nolecule type: DNA
A.Rolecule type: DNA
A.Rolecule type: DNA
A.Residues: 1-133 <CAS>
A.Residues: 1-133 <CAS>
A.Residues: 1-133 <CAS>
A.Residues: GB:L33715; NID:g497610; PIDN:AAA91564.1; PID:g497611
A.Note: authors translated the codon GTT for residue 119 as Arg, and GTC
R.Nakamura, M.; Xavier, R.M.; Tsunematsu, T.; Tanigawa, Y.
Proc. Natl. Acad. Sci. U.S.A. 92, 3463-3467, 1995
A.Title: Molecular cloning and characterization of a cDNA encoding monocl
A.Reference number: I59368; MUID:95241522; PMID:7724584
A.Accession: I59368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C:Species: Mus musculus (house mouse)
C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change
C:Accession: 148346; A56532; T59368; S21452
R.Michiels, L.; Van der Rauwelaert, E.; Van Hasselt, F.; Kas, K.
Oncogene 8, 2537-2546, 1993
A:Title: fau cDNA encodes a ubiquitin-like-S30 fusion protein an A:Reference number: 137387; MUID:93368957; PMID:8395683
A:Accession: 148346
A:Status: preliminary: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: fau
A;Gene: fau
A;Gene: fau
A;Introns: 25/3; 74/1; 92/3
A;Introns: 25/3; 74/1; 92/3
C;Superfamily: unassigned ubiquitin-related proteins; ubiquitin homology
C;Keywords: protein biosynthesis; ribosome
F;1-74/Domain: ubiquitin homology <UBH>
F;75-133/Product: ribosomal protein S30, cytosolic #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:x65923; NID:g31302; PIDN:CAA46716.1; PID:g31303
R;Vladimirov, S.N.; Ivanov, A.V.; Karpova, G.G.; Musolyamov, A.K.; Egorov, T.A.; Thiede, Eur. J. Biochem. 239, 144-149, 1996
A;Title: Characterization of the human small-ribosomal-subunit proteins by N-terminal and A;Reference number: S68911; MUID:96305378; PMID:8706699
A;Accession: S68911
A;Molecule type: protein
A;Residues: 75-99 <VLA>
C;Genetics:
                                                                                  A;Gene: fau
A;Introns: 25/3; 74/1; 92/3
C;Superfamily: unassigned ul
F;1-74/Domain: ubiquitin hor
                                                                                                                                                                                  A;Cross-references: GB:D26610; NID:g1060926; C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Casteels, D.; Poirier, C.;
Genomics 25, 291-294, 1995
A;Title: The mouse Fau gene:
A;Reference number: A5632; N
A;Accession: A56532
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A;Accession: I37387
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-133 <RES>
                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-133 < RE2>
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                                                                                                                                                                                                                                                                            A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:X65922; NID:g50949; PIDN:CAA46715.1; R;Casteels, D.; Poirier, C.; Guenet, J.L.; Merregaert, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Residues: 1-133 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule
Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 KVHGSLARAGKVRGQTPKVAKQEKKKKKTGRAKRRMQYNRRFVNVVPTFGKKKGPNANS 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   preliminary; translated from type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KVHGSLARAGKVRGQTPKVAKQEKKKKKTGRAKRRMQYNRRFVNVVPTFGKKKGPNANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      names: gene fau protein; monoclonal nonspecific suppressor factor
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                                                                                       ubiquitin homology
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                                                                                                                ubiquitin-related
                   100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : genomic structure, chromosomal MUID:95293388; PMID:7774934
                   .0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                          <UBH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 59;
Pred. No.
                   Score
Pred.
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                   No.
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                                                                                                             proteins;
                   DB 2;
5.2e-52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.2e-52;
                                                                                                                                                                                                          PIDN:BAA05655.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
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                                                                                                           ubiquitin
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C;Genetics:
A;Gene: AT4g29390
A;Map position: 4
                                                                                                                                                                                                                                                                                                                            RIBOSOMAL PROTEIN S30 homolog [imported] - Arabidopsis thaliana (species: Arabidopsis thaliana (mouse-ear cress) C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change C;Accession: H85342
                                                                                                                                                                                             A;Reference number: A85001;
A;Accession: H85342
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-62 <STO>
                                                                                                                                                                                                                                                                                               R; anonymous, The Euro
Nature 402, 769-777,
                                                                                                                                                                                                                                                                A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana A;Reference number: A85001; MUID:20083488; PMID:10617198
                                                                                                                                                                                A; Cross-references:
                                                               Query Match
Best Local S
Matches 22
                             1 KVHGSLARAGKVRGQTPKVAKQ 22
KVHGSLARAGKVRGQTPKVAKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                              59;
                                                               Similarity 100 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                 European Union Arabidopsis Genome Sequencing Consortium, 77, 1999
                                                                                                                                                                                 GB:NC_001268;
                                                                            37.3%;
24
                                                               0;
                                                               Score 22; DB; Pred. No. 4.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0,
                                                                                                                                                                                NID:g7269837;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                               16-Feb-2001 #text_change 16-Feb-2001
                                                                            DB 2;
4.3e-1
                                                                                                                                                                                 PIDN:CAB79697.1;
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                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                  The Cold
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A;Title: Sequence and analysis of chromosome 2
A;Reference number: A84420; MUID:20083487; PMII
A;Accession: F984580
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-68 <STO>
A;Cross-references: GB:AE002093; NID:93687243;
C:Genetics:
A;Gene: At2g19750
A;Map position: 2
C:Superfamily: yeast ribosomal protein S30.e C; Species: Homo sapiens (man) C; Date: 06-Feb-1995 #sequence C; Accession: S38383 40S ribosomal protein S30 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 17-May-2002 C;Accession: F84580 euss, D.; Nierman, W.C.; V Nature 402, 761-768, 1999 R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter SEB4B protein -Query Match Best Local S Matches 22 KVHGSLARAGKVRGQTPKVAKQ 22 Similarity human (fragment) Gupta, Conservative nd analysis of chromosome 2 of the plant Arabidopsis thaliana A84420; MUID:20083487; PMID:10617197 #sequence\_revision A.; Terworst, 37.3%; 5c. 100.0%; Pr 30 Score 22; Pred. No. NID: g3687243; PIDN: AAC62141.1; Mismatches G 06-Feb-1995 DB 2; I 4.7e-15; #text\_change 0 Length 68 GSPDB:GN00139 0, Gaps 0

C.Y

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A; Experimental source: C; Genetics:
                                                                                                                                                                                                      R;Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, ; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, Science 282, 1126-1132, 2009.
A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum. A;Reference number: A71600; MUID:99021743; PMID:9804551
A;Accession: A71604
                                                                                                                                                                                                                                                                                                                                    ribosomal protein S30 PFB0885w - malaria parasite (Plasmodium falciparum) C;Species: Plasmodium falciparum C;Species: Plasmodium falciparum C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 13-Aug-1999 C;Accession: A71604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Experimental source; C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 24-Nov-1999
C:Accession: T15642
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C;Superfamily: unassigned ubiquitin-related proteins; ubiquitin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:U53148; NID:g1255375; PID:g1255381; PIDN:AAB37076.1; GSPDB:GN0(A;Experimental source: strain Bristol N2; clone C26F1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Description: The sequence
A;Reference number: Z18381
A;Accession: T15642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Geisel, C.; Stellyes, L.; Bradshaw, H.
submitted to the EMBL Data Library, March 1996
A;Description: The sequence of C. elegans cosmid C26F1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-229 < RUE>
A; Cross-references: EMBL: X75315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: S38382
A; Accession: S38383
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                                                                                                                              A;Cross-references:
                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-58 <GAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Gene: CESP:C26F1.4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein C26F1.4 - Caenorhabditis elegans
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    Query Match
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mes 13; Conserv
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                                         yeast
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llarity 100.0%; Pred. No. 1.3e-12;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                              GB
                                       ribosomal protein
                                                                                                      clone 3D7
                                                                                                                                                                                         nucleic acid
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                                                                                                                         GB:AE001362;
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Score 12;
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                                                                                                                                                                                      sequence not shown;
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  DB
                                                                                                                         NID: g3845298; PIDN: AAC71966.1; PID: g38453
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Length 58;
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                                                                                                                                                                                    translation not shown
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A; Molecule type: DNA
A; Residues: 1-63 <BAK>
                                                                                                                                                                                                                                                                  R:Baker, R.T.; Williamson, N.A.; Wettenhall, R.E.H. J. Biol. Chem. 271, 13549-13555, 1996
A;Title: The yeast homolog of mammalian ribosomal protein A;Reference number: S70774; MUID:96278780; PMID:8662789
A;Accession: S70775
                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:Z75090; GSPDB:GN00015; MIPS:YOR182c; NID:g1420438; PIDN:CAA:A;Experimental source: strain S288C
A;Genetics: YS30B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ribosomal protein S30.e, cytosolic - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein 04725; protein YLR287c-a; protein YOR182c
C;Species: Saccharomyces cerevisiae
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C;Accession: S67074; S70775; S70776; S70774
R;Hughes, B.; Pohl, T.M.
R;Hughes, B.; Pohl, T.M.
submitted to the Protein Sequence Database, July 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ρy
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A; Introns: 13/3; 56/3
C; Superfamily: yeast
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A; Residues: 1-61 <LYN>
A; Cross-references: EM
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A; Accession: T39834
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A; Molecule type: protein A; Residues: 2-63 < BA3>
                                                                                                             A; Molecule type: mRNA
A; Residues: 1-63 <BAW>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 02-Jun-2000
                                              A; Accession: S70774
                                                                     A; Genetics: YS30A
                                                                                   A; Cross-references: EMBL: U48699;
                                                                                                                                                            A; Accession:
                                                                                                                                                                                   A; Genetics: YS30A
                                                                                                                                                                                                   A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-63 < HUG>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:ALO21839; PIDN:CAA17057.2; GSPDB:GN00067; SPDB:SPBC19G7.03c
A;Experimental source: strain 972h-; cosmid c19G7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary; translated from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ribosomal protein s30 - fission yeast (Schizosaccharomyces pombe)
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Best Local S
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mes 12; Conserv
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; Pred. No.
                                                                                          NID: g1256750;
                                                                                                                                                                                                      NID:g1256752;
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4.8e-05;
                                                                                                                                                                                                      PIDN: AAC49317.1;
                                                                                          PIDN: AAC49316.1; PID: g1256751
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:RPS30B; MIPS:YOR182c

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A; Molecule type: DNA
A; Residues: 1-134 <LA1>
C; Genetics:
A; Gene: hns
C; Function:
A; Description: binds doul
C; Superfamily: DNA-binding;
C; Keywords: DNA binding;
                                                                                                                                                                                                                   A;14 Teana, A.; Falconi, M.; Scarlato, V.; Lammi, M.; Pon, C.L.
FEBS Lett. 244, 34-38, 1989
A;Title: Characterization of the structural genes for the DNA-binding protein H-NS
A;Reference number: S02775; MUID:89171270; PMID:2494066
A;Accession: S02776
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A;Map position: 15R
A;Introns: 1/3
C;Genetics: <YS30A>
A;Gene: SGD:RPS30A; N
A;Cross-references: 1
                                                                                                                                                                                                                                                                                                             C:Species: Proteus vulgaris
C:Date: 28-Feb-1990 #sequence_revision
C:Accession: S02776
                                                                                                                                                                                                      A; Status: not compared with
                                                                                                                                                                                                                                                                                                                                            DNA-binding protein H-NS - Proteus vulgaris C:Species: Proteus vulgaris
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R:Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R. J. Bacteriol. 183, 4823-4838, 2001

A:Title: Genome Sequence and Comparative Analysis of the A;Reference number: A96900; MUID:21359325; PMID:21359325

A:Accession: A97094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     uncharacterized protein, YJDF B. subtilis ortholog [imported] - Clostridium acetobutylic C;Species: Clostridium acetobutylicum C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001 C;Accession: A97094
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A:Introns: 1/3
A:Introns: 1/3
C:Superfamily: yeast ribosomal protein S30.e
C:Keywords: cytosol; protein biosynthesis; ribosome
F;2-63/Product: ribosomal protein S30.e, cytosolic #status experimental <MAT>
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A; Residues: 1-135 < KUR>
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Matches 12
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Best Local
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     Local Similarity
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                                                                   binds double-stranded DNA; influences DNA-binding protein H-NS
                                                        binding;
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MIPS:YLR287c-a;
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                                                    transcription regulation
   11.9%;
100.0%;
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                                                                                                                                                                                                    conceptual translation
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Score 7;
Pred. No.
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Pred. No. 0.9
0; Mismatches
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DB 2;
lo. 9.8;
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nucleoporin p62 homolog - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 05-Nov-1999
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I52523
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E84782
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A; Residues: 1-199 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana A;Reference number: A84420; MUID:20083487; PMID:10617197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable homeodomain transcription factor [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001 C;Accession: E84782
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A;Experimental source: strain R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein - Deinococcus radiodurans (strain R1)
C; Species: Deinococcus radiodurans
C; Species: Deinococcus radiodurans
C; Date: 03; Os-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C; Accession: B75305
R; White, 0.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Do., M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zald S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 402, 761-768, 1999
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A; Residues: 1-154 <WHI>
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                                                                                                                                          68 QEKKKKK 74
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position: 2
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7; Conserv
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                                                                                                                                                                                                       11.9%;
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T.; Zalewski,
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Ritheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A.Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A.;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A.;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A.;Reference number: A86141; MUID:21016719; PMID:11130712

A.;Rocession: H86318

A.;Residues: 1-233 <STO>

A.Residues: 1-233 <STO>

A.RESIGUES: 1-235 <STO>

A.RESIGUES: 1-235 <ARRESIGNED: ARRESIGUES: 1-245 ARRESIGUES: 1-2
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R;Wang, Z.Q.; Akmal, K.M.; Kim, K.H.
Biol. Reprod. 51, 1022-1030, 1994
A;Title: An unusual nucleoporin-related messenger ribonucleic acid is present in A;Reference number: I52523; MUID:95151924; PMID:7849178
A;Accession: I52523
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Mesidues: 1-215 <RES>
A;Molecule type: mRNA
A;Mesidues: 1-215 <RES>
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R. Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, i. Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                         protein 60S ribosomal protein L6 F2P9.8 [imported] - Arabidopsis thaliana c;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 C;Accession: D96768 R;TheoLogis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H ansen, N.F.; Hughes, B.; Hulzar, L. Nature 408, 816-820, 2000
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C;Genetics:
A;Map position: 1
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100.0%;
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Pred. No.
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submitted to the Protein Sequence Databa
A; Reference number: Z24376
A; Accession: T47174
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-283 <AAA>
A; Cross references: EMBL: AL162072
A; Experimental source: adult melanoma (MC; Genetics: DKFZp7621166.1
C; Superfamily: unassigned WD repeat prot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Genetics:
A; Gene: F2P9.7
A; Map position:
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A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzi, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tall, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A; Accession: E96768
A; Accession: E96768
A; Status: preliminary
A, Molecule trace, Nua
                                                                                                                                                                                                                                                                                                                                  hypothetical protein DKFZp762I166.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 02-Sep-2000
C;Accession: T47174
R;Bloecker, H.; Boecher, M.; Brandt, P.; Mewes, H.W.; Weil, B.; Wiemann, S.
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A;Molecule type: DNA
A;Residues: 1-233 <STO>
A;Residues: 1-233 <STO>
A;Cross-references: GB:AE005173; NID:g7109467; PIDN:AAF36731.1; GSPDB:GN00141
C;Genetics:
A;Gene: F299.8
A;Map position: 1
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A; Residues: 1-233 <STO>
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Best Local (
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                                                                      unassigned WD repeat proteins; WD repeat homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GB:AE005173; NID:g7109466; PIDN:AAF36730.1; GSPDB:GN00141
                                                                                                                                                                                                                                                                                                              Sequence Database,
11.9%;
100.0%;
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DB 2;
o. 18;
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Similarity

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probable ABC-type transport system ATP-binding protein - C;Species: Streptomyces coelicolor C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_C;Accession: T36154
R;Seeger, K.; Harris, D.; James, K.D.; Parkhill, J.; Barr
                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein C32A3.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T19629
R;Thomas, K.
submitted to the EMBL Data Library, February 1995
A;Reference number: Z19154
A;Accession: T19629
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T19629
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                                                                                                                                                                                                                                                                      A; Map position: 3
A; Introns: 47/3; 79/3;
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A;Experimental source: clone C32A3
                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated A;Molecule type: DNA A;Residues: 1-346 <WIL>
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C;Superfamily: conserved hypothetical protein HI0963
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 riboflavin kinase - Aquifex aeolicus
C;Specias: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 20-Sep-1999
C;Accession: D70313
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A; Residues: 1-314 <AQF>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R; Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.;
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                                                           Streptomyces coelicolor
 B.G.;
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Best Loc
Matches
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submitted to the EMBL Data Library,
A; Reference number: Z21598
A; Accession: T36154
A; Status: preliminary; translated fi
A; Molecule type: DNA
A; Residues: 1-424 <SEE>
A; Cross-references: EMBL:AL096852; I
A; Cross-references: EMBL:AL096852; I
                                                                                                                   A;Status: precamble type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-710 <SCH> A;Cross-references: EMBL:AL356173; GSPDB:GN00116; NCSP:B14D6.680 A;Cross-references: BAC clone B14D6; strain OR74A
                                                                             A; Introns: 422/1
                                                                                                                                                                                                                                                                                           R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, submitted to the Protein Sequence Database, May 2000
                                                                                                                                                                                                                                                                                                                                    C;Species: Neurospora crassa
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
C;Accession: T49516
                                                                                                                                                                                                                                                                                                                                                                                           Atu related protein [imported] - Neu N; Alternate names: protein B14D6.680
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C;Superfamily: phage P22 gene 12 protein
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A; Molecule type: DNA
A; Residues: 1-454 <STO>
A; Cross-references: GB: AP001520; GB: BA0000004; NID: g10176401; PIDN: BAB07748.1;
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A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodu: A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: E84153
                                                                                                   A; Map position:
                                                                                                                                                                                                                                                         A; Reference number: Z25022
A; Accession: T49516
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Matches 7
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                      Local
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7; Conserv
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11.9%;
llarity 100.0%;
Conservative
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ce: strain A3(2)
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100.0%; Pr
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                  Score 7; Pred. No.
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Pred. No.
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27;
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25;
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                                  Length 710;
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A; Molecule type: mRNA
A; Residues: 1-1254 <SNE>
A; Residues: 1-1254 <SNE>
A; Cross-references: GB:L04599; NID:g290619; PIDN:AAA42990.1; PID:g290621
C; Superfamily: togavirus structural polyprotein
C; Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein
F; 1-274/product: coat protein #status predicted <CTP>
F: 275-333/product: membrane glycoprotein E3 #status predicted <MG3>
F; 334-756/product: membrane glycoprotein E2 #status predicted <MG2>
F; 775-812/product: fx protein #status predicted <TM1>
F: 75-812/product: fx protein #status predicted <TM2>
F; 794-813/Domain: transmembrane #status predicted <TM3>
F; 813-1254/product: membrane glycoprotein E1 #status predicted <MG1>
F; 813-1254/product: membrane #status predicted <TM3>
F: 47,285,651,946/Binding site: carbohydrate (Asn) (covalent) #status predic
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A;Map position: 4
C;Superfamily: unassigned
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RESULT
B71619
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J. Gen. Virol. 74, 519-523, 1993
A:Title: Molecular evidence that epizootic Venezuelan equine encephalitis (VEE) I-AB
A:Reference number: JQ1978; MUID:93187617; PMID:8445371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              structural polyprotein - Venezuelan equine encephalitis virus (subtype I, strain MenaII) N;Contains: 6K protein; coat protein; membrane glycoprotein E1; membrane glycoprotein E2 C;Species: Venezuelan equine encephalitis virus C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 16-Jul-1999
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A; Residues: 1-863 <STO>
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C;Accession: B69830

R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber R;Kunst, F.; Ogasawara, N.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; C.; Broni, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, Nature 390, 249-256, 1997

A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galizzi, A.; Galizeth, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, T.; Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino, A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauthors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauthors: Schleich, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanil, A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se
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A; Map po
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A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum. A;Reference number: A71600; MUID:99021743; PMID:9804551
A;Accession: B71619
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submitted to the EMBL Data Library, November 1995
a-negoription: The sequence of C. elegans cosmid (
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T28799
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C; Species: Bacillus subtilis
C; Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
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A; Reference number: Z20525
A; Accession: T28799
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A;Residues: 1-2539 <GAR>
A;Residues: 1-2539 <GAR>
A;Cross-references: GB:AE001384; GB:AE001362; NID:g3845139; PIDN:AAC71845.1; PID:g384
A;Experimental source: clone 3D7
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A;Experimental source: strain Bristol N2; clone C16E9
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A; Residues: 1-46 <GEI>
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C; Genetics:
A; Map position: 3
A; Introns: 31/3
A; Note: T22K7.120
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C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C;Accession: H97135
R;Nolling, J; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gib;
Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4338, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: H97135
                                                                                              hypothetical protein T22K7.120 - Arabidopsis thaliana
("Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C;Accession: T47434
R;Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Rudd, S
submitted to the Protein Sequence Database, April 2000
A;Reference number: Z24459
A;Accession: T47434
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-74 (*RIE)
A;Cross-references: EMBL:AL138641
A;Experimental source: cultivar Columbia; BAC clone T22K7
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A; Residues: 1-70 < KUR>
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A; Gene: yhfD
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A; Residues: 1-67 < KUN>
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N;Alternate names: ribosomal protein BS21
C;Species: Bacillus subtilis
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jul-2000
C;Accession: S66013; S11368; A69701
R;Ogasawara, N.; Nakai, S.; Yoshikawa, H.
DNA Res. 1, 1-14, 1994
A;Title: Systematic sequencing of the 180 kilobase region of the Bacillus su
A;Reference number: S65967; MUID:96051385; PMID:7584024
A;Accession: S66013
A;Experimental source: strain 168
A;Note: 20-Asp was also found
A;Note: 20-Asp was also found
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,
Nature 390, 249-256, 1997
                                                                                                                                                                            A;Experimental source: strain 168
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1993
R;Higo, K.I.; Otaka, E.; Osawa, S.
MOI. Gen. Genet. 185, 239-244, 1982
A;Title: Purification and characterization of 30S ribosomal proteins from Bacillus su A;Reference number: S09561; MUID:82219212; PMID:6806564
A;Accession: S11368
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Query Match

10.2%;

Score

6,

DВ <u>ب</u>

Length

A;Authors: Foulger, D.; Fritz, C.; iech, J.; Harwood, C.R.; Henaut, A

.; Fujita, M.; Fujita, Y.; Fuma, A.; Hilbert, H.; Holsappel, S.;

S.; Galizzi, Hosono, S.;

Hullo,

A.; Gal

A; Molecule type: protein A; Residues: 4-26 <HIG>

A; Cross-references: EMBL: D26185; NID: 9467326; PIDN: BAA05219.1; PID: 9467373

acid sequence not shown; translation not shown

Bacillus subtilis

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A; Molecule type: DNA A; Residues: 1-81 <OGA> A; Status: nucleic

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                                                                                                        A; Map position: 1
C; Superfamily: exodeoxyribonuclease VII
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Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae. A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: B82267
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B82267
                                                                                                                                     A; Gene:
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C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
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                        5 SLARAG
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transcription regulator XFa0057 [imported] - Xylella fastidiosa (strain 9a5c) C.Species: Xylella fastidiosa C.Species: Xylella fastidiosa C.Date: 18 Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000 C.Accession: H82867
R.anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleo Nature 406, 151-157, 2000
A.Yiltle: The genome sequence of the plant pathogen Xylella fastidiosa.
A.Yatle: The genome sequence of the plant pathogen Xylella fastidiosa.
A.Reference number: A82515; MUID:20365717; PMID:10910347
A.Rocession: H82867
A.Rocession: H82867
A.Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein SCE19A.11c - Streptomyces coelicolor C; Species: Streptomyces coelicolor C; Species: Streptomyces coelicolor C; Date: 03.0-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 19-Jan-2001 C; Accession: T36134
R; Seeger, K.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, submitted to the EMBL Data Library, July 1999
A; Reference number: Z21598
A; Accession: T36134
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A;Gene: rpsR
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A;Residues: 1-81 <KUN>
A;Cross-references: GB:Z99124; GB:AL009126; NID:g2636442; PIDN:CAB16126.1; PID:g2636636
A;Experimental source: strain 168
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A; Residues: 1-92 <SEE>
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family: probable sulfur carrier protein slr0821
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6; Conserv
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Pred. No.
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C;Decles: Arabidopsis thaliana (mouse-ear cress)
C;Decles: Arabidopsis thaliana (mouse-ear cress)
C;Decles: Arabidopsis thaliana (mouse-ear cress)
C;Date: (0.2 mar-2001 *sequence_revision 0.2 mar-2001 *text_change 31-mar-2001 C;Accession: H96585
C;Date: (0.2 mar-2001 *sequence_revision 0.2 mar-2001 *text_change 31-mar-2001 C;Accession: H96585
C;Date: (0.2 mar-2001 *sequence_revision 0.2 mar-2001 *text_change 31-mar-2001 C;Accession: H96585
C;Date: (0.2 mar-2001 *sequence, v.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dansen, N.E.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dansen, N.E.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, T.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Accession: H96585
A;Accession: H96585
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A; Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fi J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Kriteger, J.E.; Kuramae, E.E.; Le chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, A.Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C., F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawe, A.; Sauthors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L., A; Reference number: A59328
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A; Residues: 1-92 <SIM>
A; Residues: 1-92 <SIM>
A; Cross-references: GB: AE003851; NID: g9112238; PIDN: AAF85625.1; GSPDB: GN00130; XFSC:)
A; Experimental source: strain 9a5c
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A; Note: plasmid pXF5.1
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A; Residues: 1-98 <STO>
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                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                             GB:AE005173; NID:g4585983; PIDN:AAD25619.1; GSPDB:GN00141
                                                                                                                     10.2%; Score 6; DB 2
100.0%; Pred. No. 76;
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.2%; Score 6; 1
100.0%; Pred. No.
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72;
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                                                                                                                                                                                Length 98;
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Maiti, R.; Marzie
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T07078

cold stress protein SRC1 - soybean
C:Species: Glycine max (soybean)
C:Date: 30-Apr-1999 #sequence\_revis
C:Accession: T07078

#sequence\_revision

30-Apr-1999 #text\_change

20-Jun-2000

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hypothetical protein 105 (grm 3' region) - Micromonospora purpurea (fragment) C;SpecLes: Micromonospora purpurea (c;Date: 30-Sep-1991 *sequence_revision 30-Sep-1991 *text_change 28-Oct-1994 C;Accession: PW0017 R;Kelemen, G.H.; Cundliffe, E.; Financsek, I. Gene 98, 53-60, 1991 Gene 98, 53-60, 1991 A;Reference number: JG0017; MUID:91192615; PMID:2013410 A;Reference number: JG0017; MUID:91192615; PMID:2013410 A;Accession: PW0017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           virulence-associated protein, probable [imported] - Caulobacter crescentus c;Species: Caulobacter crescentus C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001 C;Accession: C87604 R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M., Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: C87604
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A;Experimental source: cultivar Kitamusume
C;Genetics:
                                                                       A; Cross-references: GB:M55520
A; Note: the authors translated
C; Keywords: antibiotic resisti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:AE005673; NID:g13424481; PIDN:AAK24831.1; GSPDB:GN00148 C;Genetics: A;Gene: CC2867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: src1
C;Superfamily: cold stress
C;Keywords: cold shock
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Plant Sci. 123, 93-104, 1997
A;Title: CDNA sequence analysis and expression of two
A;Reference number: Z15902
A;Accession: T07078
                                                                                                                           A; Molecule type: DNA
A; Residues: 1-105 <KEL>
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A; Residues: 1-104 <S
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A;Molecule type: mRNA
A;Residues: 1-102 <TAK>
   Matches
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les 6; Conserv
                    Local
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                                                                                          authors translated
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   Similarity 6; Conser
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6; Conser
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 Llarity 100.0%;
Conservative 0;
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 Score 6; DB 2;
Pred. No. 81;
0; Mismatches
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Pred. No.
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Pred. No.
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                                                                                          and
                                                                                 RyBarrell, B.G.
RyBarrell, B.G.
submitted to the EMBL Data
submitted number: S47445
                                                                                                                                        hypothetical protein YMR290w-a - yeast C;Species: Saccharomyces cerevisiee C;Date: 23-Aug-1996 #sequence_revision C;Accession: $69849
                                                                                                                                                                                                                RESULT 42
S69849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Accession: S59536
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-106 <CAI>
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A;Cross-references: EMBL:L39005; NID:g625154; PIDN:AAA99963.1; PID:g625155
A;Experimental source: seedling; tissue type leaf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Cai, Q.; Moore, G.A.; Guy, C.L.
Plant Mol. Biol. 29, 11-23, 1995
A;Title: An unusual group 2 LEA gene family in citrus responsive
A;Reference number: S59534; MUID:96017610; PMID:7579157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Species: Poncirus
C; Date: 19-Mar-1997
C; Accession: S59536
                                    A; Molecule type: DNA .
A; Residues: 1-115 <BAR>
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C;Keywords: cold shock
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Gene 98, 53-60, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Micromonospora sp.
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 28-Oct-1994
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PW0018
                  A; Cross-references: EMBL: X80836;
                                                                    A; Accession: S69849
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A; Residues: 1-105 <KEL>
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||||||
11 SLARAG
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Poncirus trifoliata
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100.0%; Pr
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                    MIPS:YMR290w-a
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                                                                                                                                                                                           yeast (Saccharomyces cerevisiae)
                                                                                                       August 1994
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Pred. No. 81;
Mismatches
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Gaps

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Length 106 Indels

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low temperature

residues

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31,

and 37

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genes

from Micromonosp

Length 105

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Indels

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Gaps

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A;Cross·references: GB:AE001259; GB:AE000520; NID:g3323209; PIDN:AAC65861.1; PID:g332322
A;Experimental source: strain Nichols
C;Genetics:
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                                                                                                                                                                                                                                                                                                                         R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, they, L.; Weidman, J.; Smith, H.O.; Venter, J.C. Science 281, 375-388, 1998
                                                                                                                                                                                                                                                                                                                                                                                             probable ribosomal protein L19 (rplS) - syphilis spirochete
C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 13-Aug-1999
C;Accession: B71268
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A; Residues: 1-117 <STO>
A; Cross-references: GB: AE002093; NID: g4874310; PIDN: AAD31372.1; GSPDB: GN00139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:10617197 A;Accession: H84651
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                                                                                                                                 A;Gene: TP0909
C;Superfamily: Escherichia coli ribosomal protein
                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-123 <COL>
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                                                                 Conservative
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ribosomal protein S25, cytosolic [validated] - rat c;Species: Rattus norvegicus (Norway rat) C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jul-2000 C;Accession: A38965; S17353 R;Chan, Y.L.; Wool, I.G.
                                                                                                                                                                                                                                            A;Cross-references: EMBL:X62482; NID:g57723; PIDN:CAA44349.1; PID:g57724 A;Note: the protein is designated as ribosomal protein S25 by comparison C;Superfamily: rat ribosomal protein S25 C;Keywords: protein biosynthesis; ribosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 45
R3RT25
                                                                                                                                                                                                                                                                                                                                                                 Biochem. Biophys. Res. Commun. 186, 1688-1693, 1992
A;Title: The primary structure of rat ribosomal protein
A;Reference number: JH0691; MUID:92378645; PMID:1354961
A;Accession: A38969
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Search completed: February
Job time : 21 secs
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      Q9h5v4 homo sapien
Q9jj24 mus musculu
Q920w8 mus musculu
Q920w7 mus spicile
Q91v99 mus musculu
Q90yp1 ictalurus p
Q9m0e4 arabidopsis
Q15351 homo sapien
Q9vdh8 drosophila
Q18231 caenorhabdi
Q862q1 spodoptera
Q9sej0 arabidopsis
Q97ir7 clostridium
Q91657 proteus mir
Q91se5 deinococus
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## ALIGNMENTS

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Matches 59
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Q9H5V4;
Q1-MAR-2001 (TrEMBLrel. 16, Created)
Q1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CDNA: FLJ22986 fis, clone KAT11742.
                                                                                                                                                                   Watanabe K., Kumagai A., Itakura S., Yamazaki M., Tashir Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T. Nakamura Y., Isogai T., Sugano S.;

"NEDO human cDNA sequencing project.";

Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AKO26539; BAB15515.1; -.

HSSP; PO2248; IUBI
InterPro; IPRO00626; Ubiquitin.

Pfam; PF00240; ubiquitin.
                                                                                                      PRINTS; PRO0348; UBIQUITIN.
SMART; SM00213; UBQ; 1.
PROSITE; PS00299; UBIQUITIN_1;
PROSITE; PS50053; UBIQUITIN_2;
SEQUENCE 133 AA; 14390 MW;
                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
  75
1 Similarity 100. 59; Conservative
                                                               100.0%;
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                                                   Score 59; DB 4; Pred. No. 3.5e-56; Mismatches 0;
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5D2F81F2A355B559 CRC64;
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anaka T.,
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RESULT

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Q920W8;
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                  Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
EMBL; AF147745; AAF80246.1; -.
EMBL; AK008466; BAB25684.1; -.
EMBL; AK008355; BAB22034.1; -.
                                          Q920W8
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Q9JJ24;
Q9JJ24;
Q1-CCT-2000 (TrEMBLrel. 15, Created)
Q1-CCT-2000 (TrEMBLrel. 15, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MONOCLONAL non-specific suppressor factor beta (Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously expressed) (fox
                                                                                                                                                                                                                                                                                                             PRINTS; PR00348; UBIQUITIN. SMART; SM00213; UBQ; 1.
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Nie G. Y., Li Y., Salamonsen L.A., Clements J.A., Findlay J.K.;
"Identification of monoclonal non-specific suppressor factor beta
one of the genes differentially expressed at implantation sites
compared to interimplantation sites in the mouse uterus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kawai J., Shinagawa A., Shibata K., Yoshino M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=C57BL/6J; TISSUE-SMALL INTESTINE, MEDLINE-21085660; PubMed-11217851;
                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000626; Ubiquitin. Pfam; PF00240; ubiquitin; 1.
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Mammalia; Eutheria; Rodentia;
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                                      PRT;
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Adachi J., Fukuda
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Q91V99;
Q91V99;
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                                                                                                                                                                                                                                                                                                                                           Mus spicilegus (Steppe mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                  SEQUENCE
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01-MAR-2002
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                                                                                                                                                                                                                                                              Five Mus musculus subspecies.
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"Conspicuous Differences among Gene Genealogies of 21 Nuclear (
                                                                                                                                                                                                                                                                                                STRAIN-ZBN;
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Eukaryota; Metazoa; C
Mammalia; Eutheria; R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000626; Ubiquitin. Pfam; PF00240; ubiquitin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AB039086; BAB68610.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Liu Y., Kitano T., Koide T., Shiroishi T., Moriwaki K., Saitou "Conspicuous Differences among Gene Genealogies of 21 Nuclear C Five Mus musculus subspecies.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Five Mus musculus subspecies.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
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                                                                             1 KVHGSLARAGKVRGQTPKVAKQEKKKKKTGRAKRRMQYNRRFVNVVPTFGKKKGDNANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79 KVHGSLARAGKVRGQTPKVAKQEKKKKTGRAKRRMQYNRREVNVVPTFGKKKGPNANS 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 KVHGSLARAGKVRGQTPKVAKQEKKKKKTGRAKRRMQYNRRFVNVVPTFGKKKGDNANS
                                                                                                                                                                                                                                                                                                                                                                                             protein
                                                               KVHGSLARAGKVRGQTPKVAKQEKKKKKTGRAKRRMQYNRRFVNVVPTFGKKKGPNANS 13:
                                                                                                                               Similarity
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PS50053; UBIQUITIN_2; 1.
                                                                                                                                                                  137 AA;
                                                                                                                                                                                                                                                                                                                                                                                                   t (Tremblrel. 19,
l (Tremblrel. 19,
2 (Tremblrel. 20,
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                                                                                                                   Conservative
           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                           (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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                                                                                                                                                                14787 MW;
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Rodentia;
                                                                                                                              100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14845 MW;
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Last annotation update)
         PRT;
                                                                                                                          Score 59; DB 11;
Pred. No. 3.6e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 59; DB LL,
Pred. No. 3.6e-56;
                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                              57099FF7065D8828 CRC64;
                                                                                                                                                                                                  UNKNOWN_1.
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                                                                                                                 Mismatches
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01-DEC-2001 01-DEC-2001 01-MAR-2002

(TrEMBLrel.

19, 19, 20,

Last Last

annotation sequence update)

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Best Local
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Best Local
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Q90YP1;
01-DEC-2001 (TrEMBLrel. 19, C
01-DEC-2001 (TrEMBLrel. 19, L
01-MAR-2002 (TrEMBLrel. 20, L
40S ribosomal protein S30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Five Mus musculus subspecies.";
Submitted (FEB-2000) to the EMBL/
EMBL; BAB68608.1;
EMBL; AB039084; BAB68609.1;
EMBL; AB039085; BAB68612.1;
EMBL; AB039089; BAB68612.1;
EMBL; AB039089; BAB68613.1;
EMBL; AB039099; BAB68613.1;
EMBL; AB039090; BAB68615.1;
EMBL; AB039091; BAB68615.1;
EMBL; AB039092; BAB68615.1;
InterPro; IPR000626; Ubiquitin.
Pfam; PF00240; ubiquitin; 1.
PROSITE; PS0029; UBIQUITIN_1; UN
PROSITE; PS0029; UBIQUITIN_2; 1.
                                                                                                                                                                                                                                                                                          Submitted (JUL-2001) to the EMBI
EMBL; AF402841; AAK95215.1; -.
InterPro; IPR000626; Ubiquitin.
Pfam; PF00240; ubiquitin; 1.
PROSITE; PS50053; UBIQUITIN_2; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Translational machinery of approach to the analysis of expression.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ictalurus punctatus (Channel catfish).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriforme;
Ictaluridae; Ictalurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-VARIOUS STRAINS;
Liu Y., Kitano T., Koide T., Sh
"Conspicuous Differences among
"Conspicuous Differences among
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Karsi A., Patterson A., Feng J., Liu Z.J.;
"Translational machinery of channel catfish: I. A transcriptomic approach to the analysis of 32 40S ribosomal protein genes and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
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                                                                                                                                   Local
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QYNRREVNVVPTFGKKKGPNANS
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l Similarity 100.0%;
59; Conservative 0
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23; Conser
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                                                                                                                               Score 23;
Pred. No.
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Pred. No. 3.6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UNKNOWN_1.
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                                                                                                                                                                                                                                62036BB0E72C5CAC CRC64;
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                                                                                                    Mismatches
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annotation update)
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hes 0;
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ogies of 21 N
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                                                                                                                                                           Length 133;
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KVHGSLARAGKVRGQTPKVAKQ

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Query Ma
Best Loc
Matches
                                                                                   "Arabidopsis ORF clones.";

Submitted (OCT-2001) to the EI

EMBL; AL161574; CAB79697.1;

EMBL; AB013392; BAB09885.1;

EMBL; AY052341; AAK96533.1;

EMBL; AY061910; AAL31237.1;
                                                                                                                                                                                                                                                                                                               Shinn P., Chen H., Cheuk R., Kim C.J., Koesema E., Meyers M.C., Banh J., Bowser L., Carrinci P., Dale J.M., Goldsmith A.D., Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin Neumann G., Kawai J., Lam B., Lee J.M., Liu S.X., Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick J. Tang C.C., Toriumi M., Yamada K., Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.; "Arabidopsis cDNA clones."; Shimozaki CDNA clones.";
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Mewes H.W., Lemcke K.,
Submitted (MAR-2000) t
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Ribosomal protein S30 homolog (40S ribosomal protein S30 homolog)
(At2g19750/F6F22.22).
AT4G23390
                                                                                                                                                                                      Kim C.J., Chen H., Cheuk R., Koesema E., Meyers M.C., Banh J., Bowser L., Carninci P., Chang E., Dale J.M., Goldsmith A.D., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Sat Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Structural analysis of Arabidopsis thaliana c Sequence features of the regions of 1,367,185 physically assigned Pl and TAC clones."; DNA Res. 5:203-216(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnollophyta; eddicotyledons; core evenosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                             SEQUENCE
                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Kim C.J., Chen H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tabata S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                Local
                                Match
  Similarity
22; Conserv
                                                           protein.
62 AA;
37.3%; Scilarity 100.0%; F
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                                                             6887 MW;
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he EMBL/GenBank/DDBJ
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                 Score 22;
Pred. No.
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                                                           95D8F3EB72F53F33 CRC64;
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5 bp covered
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SEB4B(HUMAN).
Homo sapiens (Human).
Homo sapiens (Human).
Thervota; Metazoa; Chordata; Ci
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S. Ashurner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Butler R.M., Bouck J., Brokstein P., Brottier P., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Dietz S.M.,
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01-MAY-2000 (TIEMBLIEL 13,
01-MAR-2002 (TIEMBLIEL 20,
CG15697 protein (RH08962p).
CG15697.
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Q15351;
Q1-NOV-1996
Q1-NOV-1996
Q1-YUN-2002
                                                                                                                                                                                                                                     Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscrephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                           MEDLINE=20196006; PubMed=10731132;
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SMART; SM00360; RRM; 1.
PROSITE; PS50102; RRM; 1.
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PROSITE; PS00030; RRM_RNP_1; UNKNOWN_1.
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"A novel murine RRM-type protein and its human homolog.
Submitted (SEP-1993) to the EMBL/GenBank/DDBJ databases
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Pred. No
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RA Fosler C., Gabrielian A.E., Carg N.S., Celbart W.M., Glasser K., Ra Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., RA Harris N.L., Havey D., Heiman T.J., Hernandez J.R., Houck J., RA Harris N.L., Havey D., Heiman T.J., Wei M.-H., Ibegwam C., RA Kinmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D., Lai X., Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D., RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T., RA Spier E., Spradling A.C., Stapleton M., Stupski M.P., Smith T., RA Williams S.M., Woodage T., Worley K.G., Weissenbach J., RA Williams S.M., Woodage T., Worley K.C., Wang A.H., Wang X., RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., RA Shue B.C., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., RA Spier E., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O., RA Schence 287:2185-2195(2000).
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Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Cou Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnst Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
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Q18231; O1-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-DEC 2001 (TrEMBLrel. 19,
                                                                                 STRAIN=BRISTOL N2;
MEDLINE=94150718; PubMed=7906398;
                                                                                                                                                Rhabditidae; pel
NCBI_TaxID=6239;
                                                                                                                                                                                 Caenorhabditis elegans
Eukaryota; Metazoa; Ner
                                                                                                                 SEQUENCE FROM N.A.
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EMBL; AY071683; AAL49305.1; --
FlyBase; FBgn0038834; CG15697.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Dresnek D., Frifan D., Frise E., George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
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? AA; 14585
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                                                                                                                                                               oda; Chromadorea; Rhabditida; Rhabditoidea;
Caenorhabditis.
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Last sequence update)
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Mismatches
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Q9S9J0
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EMBL: U53148; AAB37076.1; -.
HSSP; P02248; 1UBI.
InterPro; IPR000626; Ubiquitin.
Pfam; PF00240; ubiquitin; 1.
SMART; SM00213; UBQ; 1.
   Q9S9J0;
Q9S9J0;
01-MAY-2000
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Q962Q1; O1-DEC-2001 (TremBLrel. 19,
01-DEC-2001 (TremBLrel. 19,
01-JUN-2002 (TremBLrel. 21,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Landais I., Ogliastro M., Mita K., Nohata J., Lopez-Ferber Nonor-Cerutti M., Fournier P., Devauchelle G.; "Full-length ribosomal protein sequence from an EST library Spodoptera frugiperda cells (Sf9)."; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AF400225; AAK92197.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ribosomal protein S30.
Spodoptera frugiperda (Fall armyworm).
Spodoptera frugiperda (Fall armyworm).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Di
Noctuoidea; Noctuidae; Amphipyrinae; Spodoptera.
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STRAIN-BRISTOL N2;
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|||||||||||||||
| 72 KVHGSLARAGKVR
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                                                                                                                                                                                                                                                                         KVHGSLARAGKV
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13; Conserv
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nilarity 100.0%;
Conservative 0
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   (TrEMBLrel. (TrEMBLrel.
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                                                                                                       PRELIMINARY;
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Last sequence update)
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Created)
Last sequence update)
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Pred. No.
                                                                                                       PRT;
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C26F1.";
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Best Local :
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097IR7;
01-CCT-2001 (TrEMBLrel. 18, Created)
01-CCT-2001 (TrEMBLrel. 18, Last sequence update)
01-CCT-2001 (TrEMBLrel. 18, Last annotation update)
01-CCT-2001 (TrEMBLrel. 18, Last annotation update)
                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

STRAIN-APCC 824 / DSM 792 / VKM B-1787;

MEDLINE-21359325; PubMed-11466286;

Noelling J. Breton G. Omelchenko M.V., Makarova K.S., Zeng Q.,

Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly P.

Bennett G.N., Koonin E.V., Smith D.R.;

"Genome sequence and comparative analysis of the solvent-producinaction (183:4823-4838(2001)).

J. Bacteriol. 183:4823-4838(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Theologis A.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases
SUBL; AC007230; AAD26867.1; -.

NON_TER 309 309 AFF11D7AF877A0D1 CRC64;
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VYSOCISKAIA V.S., SCHWARTZ J.R., Yu G., Toriumi M., Lenz C.
Li J., Kremenetskaia I., Ngan I., Luros J., Gonzalez A., A
Araujo R., Chao Q., Conn L., Conway A.B., Dunn P., Hansen
Huizar L., Kim C., Palm C.J., Rowley D., Shinn P., Walker
Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.;
"Arabidopsis thaliana chromosome 1 BAC T23K8 sequence.";
                                                                                                                                                                                                         J. Bacteriol. 183:4823-4838(20

EMBL; AE007667; AAK79540.1; -.

Complete proteome.

SEQUENCE 135 AA; 16388 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia; Clostridiales; Clostridiaceae; Clostridium.
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; endicotyledons; core eudicots; Rosidae;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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T23K8.1 (Fragment).
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  124
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                                                21 KQEKKKKK
  KQEKKKKK 131
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9; Conserv
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8; Conser
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                                                                                                       Conservative (
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                                                                                                                             Score 8; 1
Pred. No.
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Pred. No.
                                                                                                                                                                                                            387D5F8D11444E7A CRC64;
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D. 0.14;
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ez A., Altafi
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RESULT 15
Q9RSE5
ID Q9RSE
AC Q9RSE
DT 01-M
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094657
1D 99465
AC 99465
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RO HMSt.
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         Query Match
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Matches 7
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Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                  MEDLINE=20036896; PubMed=10567266; White O., Elsen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Wamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D., Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                               radiodurans R1.";
Science 286:1571-1577(1999).
Science 286:02051; AAF11732.1; -.
TIGR; DR2179; -
                                                                                                  Hypothetical protein; Complete SEQUENCE 154 AA; 16181 MW;
                                                                                                                                                                                                                                   "Genome sequence of the radioresistant bacterium radiodurans R1.":
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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NCBI_TaxID=1299;
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01-OCT-2000
01-OCT-2000
01-DEC-2001
                                                                                                                                                                                                                                                                             Fraser C.M.;
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01-MAY-2000
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Pfam; PF00816; Histone_HNS; 1.
ProDom; PD007337; Histone_HNS; 1.
SMART; SM00528; HNS; 1.
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EMBL; AF240693; AAF61240.1; -.
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Coker C., Bakare O.O., Moble
"H-NS is a Repressor of the
Activator Gene urer.";
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Histone-like nucleoid structuring protein.
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11.9%; Score 7; 1
100.0%; Pred. No.
Live 0; Mismatc!
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Lin x., Kaul S., Shea T.P., Fujii C.Y., Shen M., Vanaken S.E.,
Barnstead M.E., Mason T.M., Bowman C.L., Ronning C.M., Benito I
Carrera A.J., Creasy T.H., Bell C.R., Town C.D., Nierman W.C.,
Fraser C.M., Venter J.C.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AC006282; AAD20137.2;
EMBL; AC006282; AAD20137.2;
DNA-binding; Homeobox; Nuclear protein.
SEQUENCE 173 AA; 20478 MW; 57A67DCDA47E75FF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core e
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID-3702;
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01-MAY-1999 (TrEMBLrel. 10, Created)
01-JUN-2002 (TrEMBLrel. 21, Last seq
01-JUN-2002 (TrEMBLrel. 21, Last anno
Putative DNA binding protein with ho
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Q1-OCT-2000 (TrEMBLrel. 15, Created)
Q1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
Q1-OCT-2000 (TrEMBLrel. 20, Last annotation update)
Q1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Stretchin-MLCK (Fragment).
STRN-MLCK OR CG8304 OR CG18255.
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J. Mol. Biol. 0:0-0(2000).
EMBL; AF257306; AAF90124.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FlyBase;
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157 AA;
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a Novel M
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Mismatches
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Member of the Titin/Myosin Light
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InterPro; IPR001882; Biotin_attach.
InterPro; IPR001882; Biotin_lipoyl.
InterPro; IPR000089; Biotin_lipoyl.
Pfam; PF00254; biotin_lipoyl; 1.
PRINTS; PR01071; ACCOABIOTINCC.
TIGREAMS; TIGR00531; BCCP; 1.
PROSITE; PS00188; BIOTIN; UNKNOWN_1.
NON_TER 198 199
                                                                                                                                                                                                                        Wang 2.Q., Akmal K.M., Kim K.H.;
"An unusual nucleoporin-related messenger ribonucleic in the germ cells of rat testis.";
Biol. Reprod. 51:1022-1030(1994).
                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Cloning and sequence of the aroD gene of Brucella abortus."; Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases. EMBL, AP126476; AAK27449.1; -. HSSP; P02905; 3BDO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group; Brucellaceae; Brucella.
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01-JUN-2001
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                                                                SEQUENCE
                                                                                              Biol. Reprod. 51:1022-1030
EMBL; S75997; AAB33384.1;
                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE-95151924; PubMed-7849178;
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  KKKKKTG
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                      Similarity 7; Conserv
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ilarity 100.0%;
Conservative
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                      Conservative
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                                                                                                                                                                                            Chordata;
Rodentia;
                                                              24593
                                                                                                                                                                                                                                                                                                                                                                                                                      20832 MW;
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                                                                                                                                                                                                                          protein (Fragment).
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                     Score 7; DB 1; Pred. No. 15; 0; Mismatches
                      0;
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Pred. No. 14;
0; Mismatches
                                                                                                                                                                                          Craniata; Veri
Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                      D6CB392B2D4146E2 CRC64;
                                                               098251C97A8FBD88 CRC64;
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                               DB 11;
5. 15;
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                                                                                                                                                                                            Muridae;
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                                        Length 215;
                      Indels
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                                                                                                                                                                                                      Euteleostomi;
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Q9FZ76
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O9EZ76;
O1-MAR-2001 (TIEMBLICAL 1:
01-MAR-2002 (TIEMBLICAL 1:
01-MAR-2002 (TIEMBLICAL 2:
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O9LIR5;
O1-OCT-2000 (TrEMBLrel. 15, Created)
O1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Genomic DNA, chromosome 3, BAC clone:F14013.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheopspermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M., Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H., Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J., Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H., Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
                                                                                                                                                                                                                                                                                                                                                         Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F., Altafi H., Nguyen M., Lam B., Southwick A., Miranda M., Brooks S., Buehler E., Chao Q., Chin C., Chiou J., Choi E., Gonzalez A., Howng B., Johnson-Hopson C., Khan S., Kim C., Koo T., Lee J.M., Lenz C., Liu A., Liu S., Mukharsky N., Pham P., Sakano H., Shinn P., Toriumi M., Vaysberg M., Yu G., Ecker J., Theologis A., Davis R.W.; Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
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Sequence features of the reg
TAC and BAC clones.";
DNA Res. 7:217-221(2000).
EMBL; AP001297; BAB03010.1;
                                                                                                                                                                                                                                                           SEQUENCE FROM
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta;

Spermatophyta; Magnollophyta; eddicotyledons; core eu
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Kaneko T., Kato T.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F25I16.12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20363099;
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16, Last sequence update)
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protein L6 (Putative 60S ribosomal protein
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EMBL/GenBank/DDBJ data
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RY SEALUNCY. COLLUMBIA;

RX MEDLINE=21016719; PubMed=11130712;

RX MEDLINE=21016719; PubMed=1130712;

RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

RA White O., Alonso J., Altafi H., Araujo R., Cheuk R.F., Chin C.W.,

RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,

RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,

RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,

RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,

RA Langin-Hopper S., Lee A., Lee J.M., Lerz C.A., Li J.H., Li Y.-P.,

RA Militscher J., Miranda M., Niguyen M., Nierman W.C., Osborne B.I.,

RA Militscher J., Miranda M., Niguyen M., Nierman W.C., Osborne B.I.,

RA Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

RA Sun H., Tallon L.J., Tambunga G., Torlumi M.J., Town C.D.,

RA Sun H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;

RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
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Q9C9C6;
O1-JUN-2001 (TremBLrel. 17, C:
O1-JUN-2001 (TremBLrel. 17, L:
O1-MAR-2002 (TremBLrel. 20, L:
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O1-
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EMBL; AC026338; AAF98420.1; -.
EMBL; AY054675; AAK96866.1; -.
EMBL; AY05496; AAL66911.1; -.
InterPro; IPR000915; Ribonamic Market Miranda M., Country Pram: Dro; PR000915; Ribonamic M., Carninci P., Chen L., Country Pram: Dro; PR000915; Ribonamic M., Carninci P., Chen H., Carninci P., Chen H.,
Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M., Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H., Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J., Kim C., Lin J., Liu S.x., Narusaka M., Pham P.K., Sakano H., Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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RP SEQUENCE FROM COLUMBIA;

RX MEDLINE-21016719; PubMed-11130712;

RA MEDLINE-21016719; PubMed-11130712;

RA MITHOOLOGIS A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

RA White O., Alonso J., Altafi H., Cheuk R.F., Chin C.W.,

RA Buehler E., Chan A., Cabo O., Chen H., Cheuk R.F., Chin C.W.,

RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H.,

RA Cill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,

RA Hunter J.L., Jekins J., Johnson-Hopson C., Khan S., Khaykin E.,

RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,

RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,

RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,

RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,

RA Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,

RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;

"Samuence and analysis of chromosome l of the plant Arabidopsis
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Matches 7
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Nguyen M., Karlin-Neumann G., Southwick A., Lam B., Miranda M., Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H., Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H., Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K., Ecker J., Theologis A., Davis R.W.;
                                                                                                                                                                                                                                                                                                                                Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M., Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H., Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J., Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H., Sakurai T., Satou M., Ski M., Shinn P., Yamada K., Shinozaki K., Ecker J., Theologis A., Davis R.W.; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative 60s ribosomal protein L6.
F2P9.8 OR ATIG74050.
Real-March 18 of the content of the 
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Eukaryota; Viridiplantae; Streptophyta; Embry
Spermatophyta; Magnoliophyta; eudicotyledons;
eurosids II; Brassicales; Brassicaceae; Arabi
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Q9C9C5;
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01-JUN-2001 (TrEMBLrel.
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Pfam; PF01159; Ribosomal_L6e; 1.
ProDom; PD009612; Ribosomal_L6E; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   172
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R.W.;
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RESULT : Q9AD23 ID Q9AD23 ID Q9AD23 ID Q9AD23 OF Q9AD24 
RESULT 25
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ID Q9NSX
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Matches 7
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Best Local Similarity
Matches 7; Conserv
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                                                                                          Q9NSK3 PRELIMINARY; PRT; 283 AA.
Q9NSK3;
Q1-OCT-2000 (TrEMBLrel. 15, Created)
Q1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
Q1-OCT-2000 (TrEMBLrel. 15, Last annotation update)
Hypothetical 31.4 kDa protein (Fragment).
DKFZP7621166.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";
Nature 417:141-147(2002).
EMBL; AL590463; CAC36648.1; -.
Hypothetical protein; Plasmid.
SEQUENCE 259 AA; 28708 MW; 357BF1A6821CFE5F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L., Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H., Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M., Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S., Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S., Taylor K., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K., Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomycetaceae;
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Q9AD23;
01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2002 (TrEMBLrel. 21,
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SEQUENCE
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                             Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hopwood D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                127
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nes 7; Conserv
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ilarity 100.0%;
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Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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18;
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Best Local
                                                    Riboflavin kinase.
RIBF OR AQ_139.
Aquifex aeolicus.
Bacteria; Aquificae; /
NCBI_TaxID=63363;
                                                                                                            066535;
01-AUG-1998
01-AUG-1998
01-JUN-2002
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CG3441.
                                                                                                                                                                                                                                                                                                     Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Mirada A., Mungali C.J., Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Celniker S.; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases. EMBL; ANG60340; AAL25379.1; -. FlyBase; FBgn0035092; CG3441. SEQUENCE 309 AA; 34197 MW; 620BB8A464BEF487 CRC64;
                                                                                                                                                          066535
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q95T41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bloecker H., Boecher M., Brandt P., Mewes H.W., Weil B., Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AL162072; CAB82408.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-MELANOMA;
MEDLINE-98196666; PubMed-9537320.
Deckert G., Warren P.V., Gaaster
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                             Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
                                  SEQUENCE FROM
                                                                                                                                                                                                                153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       236 GSLARAG 242
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7; Conserv
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7; Conser
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3 (TrEMBLrel.
2 (TrEMBLrel.
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ilarity 100.0%;
Conservative (
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Last sequence update)
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Last sequence update)
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Pred. No.
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                                                                  Aquificaceae;
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  Lenox A.L.,
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
"The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.";
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STRAIN-BRISTOL N2;
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans.

Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;

Rhabditidae; Peloderinae; Caenorhabditis.
  Q96GN4
                                                                                                                                                                                                                                                                                                                                                 "Direct Submission.";
Submitted (NOV-2001) to the
EMBL; AC084197; AAL00874.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 392:353-358(1998).
EMBL; AE000675; AAC06488.1; -.
InterPro; IPR002606; FAD_Synth; 1.
Pfam; PF01687; FAD_Synth; 1.
PFCDOM; PD003662; FAD_Synth; 1.
                                                                                                                                                                                                                                                                     Hypothetical protein SEQUENCE 339 AA;
                                                                                                                                                                                                                                                                                                             Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                               Waterston R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The sequence of C. elegans cosmid Y73B6BL."; Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
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Complete proteome.
SEQUENCE 314 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-BRISTOL N2;
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                                                                                                                                                                                                                                                                                                           InterPro; IPR000620; DUF6.
Pfam; PF00892; DUF6; 1.
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    PRELIMINARY;
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adamstides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Wan K.H., Dayle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Ghorit S.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Dew I., Dietz S.M.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Dew I., Dietz S.M.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Dew I., Dietz S.M.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Dew I., Dietz S.M.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Dew I., Dietz S.M.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Dew I., Dietz S.M.,
RA Cherry J.M., Comp F., Gorrell J.H., Gu Z., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeywam C.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Liang Y., Lin X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., McPherson J.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., McPherson J.,
RA Hostin A. W. McParry C. McParley T. McPherson D.,
RA Hostin A. No McParley C., McParley T., McPherson D.,
RA Hosti
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Best Local S
Matches 7
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Similar to kinesin family member 5B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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Submitted (JUN-2001) to the EMBL/GenBank/DDBJ
EMBL; BC00353; AAH09353.1; .
InterPro; IPR001752; kinesin_motor.
Pfam; PF00225; kinesin; 1.
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01-MAY-2000
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PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
ATP-binding; Coiled coil; Microtubules; Motor protein.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WEDLINE=20196006;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=10731132;
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100.0%; Pr/
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26;
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Homo.
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Milshina N.V.,

Mobarry C.,

Morris

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RESULT OLIS 694
ID 97
AC 0.1
A
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Q9S2FQ
ID Q9S
AC QS
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DT 01
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RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., PacLeb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Stupski M.P., Smith T.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Williams S.M., Woodage T., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Rubin G.M., Venter J.C.;
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
REMBL; AE003466; AAP47313.1;
P. EMBL; AE003466; AAP47313.1;
P. EMBL; AE003466; AAP47313.1;
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                                                                             O9S2F0
O9S2F0
O9S2F0;
O1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequ
O1-JUN-2002 (TrEMBLrel. 21, Last and
Putative ABC transporter ATP-binding
SCO2931 OR SCE19A.31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q15694 PRELIMINARY; PRT; 381 AA. Q15694; Q1-694; Q1-694; Q1-NOV-1996 (TrEMBLrel. 01, Created) Q1-NOV-1996 (TrEMBLrel. 08, Last sequence update) Q1-NOV-1998 (TrEMBLrel. 08, Last annotation update) Protein immuno-reactive with anti-PTH polyclonal antibodies
                             Streptomyces coelicolor. Bacteria; Firmicutes; Ac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      osteomalacia and uremia.";
Proc. Assoc. Am. Physicians 107:296-305(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-96187433; PubMed-8608414;
Kumar R., Haugen J.D., Wieben E.D., Londowski J.M.,
"Inhibitors of renal epithelial phosphate transport
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
        Actinomycetales;
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7; Conserv
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380 AA; 41734 MW;
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381 AA;
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     Streptomycineae;
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Actinobacteria; Actinobacteridae; ptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                Created)
Last sequence update)
Last annotation updat
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26;
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                                                                                                                             update)
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in tumor-induced
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RESULT 33
Q9X4J
ID Q9X4J
AC Q9X4J
AC Q9X4J
AC Q9X4J
CO DT 01-NC
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Best Local
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                                                                                                             Q9X4J1
Q9X4J1;
01-NOV-1999
01-NOV-1999
01-JUN-2002
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Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Complete genome sequence of the model coelicolor A3(2).";
Nature 417:141-147(2002).
-1 SIMILARITY: BELONGS TO THE ABC TRANEMBL; AL096852; CAB51012.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR003593; AAA_ATPase.
InterPro; IPR003439; ABC_transportr.
InterPro; IPR000644; CBS_domain.
Pfam; PF00005; ABC_tran; I.
Pfam; PF000571; CBS; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Redenbach M., Kieser H.M., Denapaite D., Eichner A., Kinashi H., Hopwood D.A.; Kinashi H., Hopwood D.A.; aset of ordered cosmids and a detailed genetic and the 8 Mb Streptomyces coelicolor A3(2) chromosome."; Mol. Microbiol. 21:77-96(1996).
                          Actinomycetales;
NCBI_TaxID=1902;
                                                                                                ProVL.
                                                                                                                                                                                                                                                                                                                                                             TIGRFAMS; TIGRO1186; proV; 1.
PROSITE; PS00211; ABC_TRANSPORTER; 1.
ATP-binding; Transport.
 SEQUENCE FROM N.A.
                                                        Bacteria;
                                                                    Streptomyces coelicolor
                                                                                    PROVI.
                                                                                                                                                                                                                                                                                                                                                                                                         ProDom; PD000006; AB
SMART; SM00382; AAA;
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James K.D., P.
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                         GSLARAG
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7; Conserv
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                                                        Firmicutes;
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424 AA; 46
                                                                                                             (TrEMBLrel. 12, (TrEMBLrel. 12, (TrEMBLrel. 21,
                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                   10
                                          Streptomycineae;
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                                                                                                                                                                                                                                                                                                                                                    46529 MW;
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                                                        Actinobacteria;
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                                                                                                           Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                    PRT;
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                                          Streptomycetaceae;
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                                                                                                                                                                                                                                                                                                          DB 16;
o. 29;
                                                        Actinobacteridae;
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                                                                                                             update)
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                                          Streptomyces.
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RESULT
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RESULT 35
Q91290
ID Q9129
AC Q9129
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Q91290 I
Q91290;
01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-C-125 / JCM 9153;
MEDLINE-20512582; Pubmed-11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., SeFuji F., Hirama C., Nakamura Y., Ogasawara N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-JUN-2002 (TrEMBLrel. 21, Replicative DNA helicase. DNAC OR BH4029.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9K5Q9
Q9K5Q9;
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Pfam; PF00772; DnaB; 1.
TIGRFAMS; TIGR00665; DnaB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                     "Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis."; Naucleic Acids Res. 28:4317-4331(2000).
                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AP001520; BAB07748.1; HSSP; P03005; 1JWE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Firmicutes; Bacillus/Clostridium
                                                                                                                                                                                                                                                                                                        Helicase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Horikoshi K.;
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281 GSLARAG 287
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7; Conserv
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nilarity 100.0%;
Conservative 0
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(TrEMBLrel.
                                       PRELIMINARY;
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Pred. No.
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                                                                                                                                                                                                                                                                                      D9D6DE17A52EAD3A CRC64;
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01-OCT-2000 (
01-OCT-2000 (
01-MAR-2002 (
                                                                                                                                                                                                                                                                           Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S., Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S.;

"NEDO human cDNA sequencing project.";

Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AK000059; BAA90916.1; -

HSSP; P17119; 3KAR.

InterPro; IPR001752; kinesin_motor.

Pfam; PF00225; kinesin_motor.

Pfam; PF00238; KINESINHEAVY.

SMART; SM00129; KISESIN MOTOR DOMAIN: INVENCEN 1

EBOGATIP: DEGOGAI: KINESIN MOTOR DOMAIN: INVENCEN 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
CDNA FLJ20052 fis, clone COL00777 (Fragment).
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

MEDIINE-95246904; PubMed-7729567;

MEDIINE-95246904; PubMed-7729567;

Coumailleau P., Billoud B., Sourrouille P., Moreau N., Angelier N.;

"Evidence for a 90 kDa heat-shock protein gene expression in the amphibian occyte.";

Dev. Biol. 168:247-258(1995).

EMBL; L32987; AAA92343.1; -.

HSSP; P07900; IYER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9NXU4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001104; Hsp90.
Pfam; PF00183; HSP90; 1.
NON_TER 1 1
SEQUENCE 542 AA; 63096 M
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Heat shock protein 90 (Fragment).
HSC90.
                                                                                                                                                          SEQUENCE
                                                                                                                                                                               ATP-binding; Coiled coil; Microtubules; NON_TER 576 576
                                                                                                                                                                                                                                 PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; UNKNOWN_1.
PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-COLON;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pleurodeles.
NCBI_TaxID=8319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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  22 QEKKKKK 28
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                                                                              Similarity
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                                                         Conservative
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100.0%; Pr
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Primates;
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Pred. No.
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                                                                                                                                                          A21BBE950F4946D6 CRC64;
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39;
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D. 37;
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InterPro; IPR003598; Bact_sens_pr_C.
InterPro; IPR003660; HAMP.
InterPro; IPR003661; His_kina.
InterPro; IPR003661; His_kina.
InterPro; IPR004359; HIS_KIN_sig.
Pfam; PF00672; HAMP; 1.
Pfam; PF02518; HATPase_c; 1.
PFam; PF00512; signal; 1.
PRINTS; PR00344; BCTRLSENSOR.
SMART; SM00307; HAMP; 1.
SMART; SM00308; HAMP; 1.
SMART; SM00308; HAMP; 1.
SMART; SM00308; HAMP; 1.
                                                                                                                                                                                                                                                                                                                                          Q9M8T5;
Q1-QCT-2000 (TrEMBLrel. 1
Q1-QCT-2000 (TrEMBLrel. 1
Q1-DEC-2001 (TrEMBLrel. 1
F13E7.12 protein.
F13E7.12.
                                                                                                                                                                                                                Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
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SEQUENCE
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STRAIN-CV. COLUMBIA;
Lin X., Kaul S., Town C.D., Benito M., Creasy T.H.,
Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., B.
Bowman C.L., White O., Nierman W.C., Fraser C.M.;
"Arabidopsis thaliana chromosome III BAC F13E7 genor
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databi
EMBL; AC018363; AAF26966.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; alpha subdivision;
Phyllobacteriaceae; Mesorhizobium.
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01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation updat
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01-OCT-2001
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EMBL; AP003005; BAB51602.1; -
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ilarity 100.0%;
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                                                genomic sequence.";
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Interpro; IPR002896; Herpes_glycop_D.
Interpro; IPR003592; LRR_out.
Interpro; IPR003592; LRR_out.
Interpro; IPR003592; LRR_out.
Interpro; IPR002290; Ser_thr_pkinase.
Interpro; IPR002290; Ser_thr_pkinase.
Interpro; IPR001245; Tyr_pkinase.
Interpro; IPR001245; Tyr_pkinase.
Interpro; IPR001245; Tyr_pkinase.
Interpro; IPR001245; Tyr_pkinase.
Interpro; IPR001245; Tyr_pkinase; 1.
Pfam; PF001537; Herpes_glycop_D; 1.
Pfam; PF001537; Herpes_glycop_D; 1.
Pfam; PF00069; Pkinase; 1.
PRINTS; PR001651; SECGEXPORT.
PRINTS; PR00109; TYRKINASE.
PRODOM; PD000001; Euk_pkinase; 1.
SMART; SM00370; LRR; 2.
SMART; SM00370; LRR; 2.
SMART; SM00370; IRR; 2.
SMART; SM00370; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00110; PROTEIN_KINASE_ST; 1.
PROSITE; PS00101; PROTEIN_KINASE_ST; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9MOD8 PRELIMINARY; PRT; 863 AA.
Q9MOD8;
Q1-OCT-2000 (TrEMBLrel. 15, Created)
Q1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Serine/threonine-specific receptor protein kinase-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPRO00875; Cecropin.
InterPro; IPRO0053; Tropomyosin.
PRINTS; PRO0194; TROPOMYOSIN.
PROSITE; PS00258; CECROPIN; UNKNC
SEQUENCE 806 AA; 91859 MW; AF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

Lennard N., Quail M., Harris B., Rajandream M.,

Mewes H.W., Lemcke K., Mayer K.F.X.;

Mewes H.W., Lemcke K., Mayer K.F.X.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ
--- SIMILARITY: BELONGS TO THE SER/THR FAMILY
EMBL; AL161575; CAB79703.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheop
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                   Transferase
SEQUENCE |
                                                                                                                                                                                                                                                    ATP-binding; Kinase;
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QEKKKKK 510
                                            QEKKKKK
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7; Conserv
                                                                                             Similarity 100.
7; Conservative
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100.08; P1
                                                                                                                                                                                                   96557
                                                                                                                                                                                                                                                    Receptor;
                                                                                                                          11.9%;
                                                                                                                                                                                                   MW:
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                                                                                                                          Score 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UNKNOWN_1.
W; AFE6F9AED5D4BBFD
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                                                                                                                                                                                                                                                    Serine/threonine-protein
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                                                                                                     Mismatches
                                                                                                                          No.
                                                                                                                       DB 10;
o. 57;
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OF PROTEIN
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Best Loc
Matches
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InterPro; IPR002548; Alpha_E1_glycop.
InterPro; IPR0002548; Alpha_E2_glycop.
InterPro; IPR0002533; Alpha_E3_glycop.
InterPro; IPR002533; Alpha_E3_glycop.
InterPro; IPR000930; Togavirin.
Pfam; PP00944; Alpha_core; 1.
Pfam; PP001589; Alpha_E1_glycop; 1.
Pfam; PP001589; Alpha_E2_glycop; 1.
Pfam; PF01563; Alpha_E2_glycop; 1.
PRNTS; PR00798; TOGAVIRIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1999 (TrEMBLrel. 12, Creation of NOV-1999 (TrEMBLrel. 12, Last 01-DEC-2001 (TrEMBLrel. 19, Last Structural polyprotein Venezuelan equine encephalitis v. Viruses; ssrNA positive-strand v. Nichesting of November 1999 (Trembuller)
          SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=98347778; PubMed=9684636;

Oberste M.S., Fraire M., Navarro R., Zepeda C., Zarate M.L.,

Coberste M.S., Kraire M., Navarro R., Zepeda C., Zarate M.L.,

Ludwig G.V., Kondig J.F., Weaver S.C., Smith J.F., Rico-Hesse R.

"Association of Venezuelan equine encephalitis virus subtype IE

"Association epizootics in Mexico.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-MENA II;
STRAIN-MENA II;
MEDLINE-99101297; PubMed-9886206;
Kinney R. M., Pfeffer M., Tsuchlya K.R., Chang G.J., Roehrig J.T.
"Nucleotide sequences of the 265 mRNAs of the viruses defining
"Nucleotide sequences of the 265 mRNAs of the viruses defining
"enezuelan equine encephalitis antigenic complex.";
Venezuelan equine encephalitis antigenic complex.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9YKD3;
01-MAY-1999 (TrEMBLrel.
01-MAY-1999 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9WC26;
Am.
                                                                                                                                                                                                                                                                                                                                                       Structural polyprotein.
Venezuelan equine encephalitis virus.
Viruses; ssRNA positive-strand viruses,
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                                                                                                                                                                                                                                                                                              NCBI_TaxID=11036;
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7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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conservative
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Last sequence
Last annotation
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POLYPROTEIN CLEAVAGE PRODUCT E3
ENVELOPE GLYCOPROTEIN 2.
6K POLYPROTEIN CLEAVAGE PRODUCT
ENVELOPE GLYCOPROTEIN 1.
MW; 0E3321D41F4DEE39 CRC64;
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Last annotation update)
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Best Local S
Matches 7
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Best Local S
Matches 7
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Q88979;
Q88979;
Q1.NOV-1996 (TrEMBLrel. 01, Created)
Q1.NOV-1996 (TrEMBLrel. 1), Last sequence (Q1.DEC-2001 (TrEMBLrel. 1), Last annotation of the control of the cont
                                                                                                                                                                             InterPro; IPR001836; Alpha_E1_glycop.
InterPro; IPR002548; Alpha_E1_glycop.
InterPro; IPR000936; Alpha_E2_glycop.
InterPro; IPR000936; Alpha_E3_glycop.
InterPro; IPR002533; Alpha_E3_glycop.
InterPro; IPR000930; Togavirin.
Pfam; PF00944; Alpha_Core; 1.
Pfam; PF001889; Alpha_E1_glycop; 1.
Pfam; PF00943; Alpha_E1_glycop; 1.
Pfam; PF00943; Alpha_E3_glycop; 1.
Pfam; PF01563; Alpha_E3_glycop; 1.
PRINTS; PR00798; TOGAVIRIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Virology 219:314-320(1996).
EMBL: U34999; AAB04683.1; -
HSSP: P03315; 1VCP.
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InterPro;
InterPro;
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J. Virol. 76:1718-1730(2002).
EMBL; U96408; AAD19216.1; -.
                                                                                                                                SEQUENCE
                                                                                                                                                          PRINTS; PR00798; Polyprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alphavirus.
NCBI_TaxID=11036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nsP3."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Complete sequence of reveals conserved and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oberste M.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=96204604; PubMed=8623548;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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InterPro;
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EMBL; AF448538;
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STRAIN-OAX142
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erPro; IPR002548; Alpha_El_glycop.
erPro; IPR002536; Alpha_E3_glycop.
erPro; IPR002533; Alpha_E3_glycop.
erPro; IPR000930; Togavirin.
m; PP00944; Alpha_core; 1.
m; PP01589; Alpha_E2_glycop; 1.
m; PP00943; Alpha_E2_glycop; 1.
m; PP00943; Alpha_E3_glycop; 1.
m; PP01563; Alpha_E3_glycop; 1.
m; PP01563; Alpha_E3_glycop; 1.
m; PP01563; Alpha_E3_glycop; 1.
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   Similarity 7; Conserv
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      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Parker M.D., Smith J.F.; uence of Venezuelan equine encephalitis virus subtype rved and hypervariable domains within the C terminus or the control of the co
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      Mismatches
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O8V291;

O1-MAR-2002 (TrEMBLrel. 20, Created)

O1-MAR-2002 (TrEMBLrel. 21, Last sequence

O1-JUN-2002 (TrEMBLrel. 21, Last annotatic

Structural polyprotein.

Venezuelan equine encephalitis virus.

Viruses; ssRNA positive-strand viruses, no
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J. Virol. 76:1718-1730(2002).
EMBL; AF448537; AAL47151.1; -
InterPro; IPR001836; Alpha_core.
InterPro; IPR002548; Alpha_E1_glycop.
InterPro; IPR002536; Alpha_E2_glycop.
InterPro; IPR000936; Alpha_E3_glycop.
InterPro; IPR000930; Togavirin.
Pfam; PF00944; Alpha_E1_glycop; 1.
Pfam; PF00948; Alpha_E1_glycop; 1.
Pfam; PF00948; Alpha_E2_glycop; 1.
Pfam; PF00948; Alpha_E2_glycop; 1.
Pfam; PF01563; Alpha_E3_glycop; 1.
PRINTS; PR00798; TOGAVIRIN.
                               SEQUENCE FROM N.A.

STRAIN-80075;

MEDLINE-21657447; PubMed-11799167;

Brault A.C., Powers A.M., Holmes E.C., Woelk C.H., Weaver S.C.;

"Positively charged amino acid substitutions in the E2 envelope
glycoprotein are associated with the emergence of venezuelan equ
encephalitis virus.";

J. Virol. 76:1718-1730(2002).

EMBL; AF448539; AAL47155.1; -.
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Venezuelan equine encephalitis virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;
Alphavirus.
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NCBI_TaxID=11036;
[1]
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SEQUENCE 1254 AA;
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InterPro; IPR000936; Alpha_E2_glycop.
InterPro; IPR000933; Alpha_E3_glycop.
InterPro; IPR000930; Togavirin.
Pfam; PF00944; Alpha_core; 1.
Pfam; PF01889; Alpha_E1_glycop; 1.
Pfam; PF01943; Alpha_E2_glycop; 1.
Pfam; PF01943; Alpha_E3_glycop; 1.
Pfam; PF01563; Alpha_E3_glycop; 1.
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OBUYH1;
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SEQUENCE 1254 A
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Venezuelan equine encephalitis virus.
Viruses; ssRNA positive-strand viruses,
                                                                                                                                                                        PRINTS; PR00798; Polyprotein.
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      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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US-09-682-358B-24
US-09-881-843A-201
US-08-851-843A-201
US-08-851-843A-210
US-08-974-549A-320
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US-08-974-549A-320
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US-08-974-94-6
US-09-427-357-479
US-08-569-749-6
PCT-US96-12860-5
PCT-US96-12860-6
US-09-082-358B-63
US-08-971-089-2
US-08-551-1860-5
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US-09-082-358B-63
US-08-9511-485-18
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                   Sequence 2, Application US/08743130A Patent No. 5871987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                             GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Sassanfar, Mandana
APPLICANT: Sallant, Paul L.
APPLICANT: Shen, Xlaoyu
APPLICANT: Tao, Nianjun
APPLICANT: Tao, Nianjun
APPLICANT: Tao, Nianjun
APPLICANT: Houman, Fariba
TITLE OF INVENTION: CANDIDA TYROSYL-TRNA SYNTHETASE
TITLE OF INVENTION: PROTEINS, NUCLEIC ACIDS AND STRAINS
                           CORRESPONDENCE
                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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    Hamilton, Brook,
                             ADDRESS:
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|            | 45                | 44               | 43               | 42                 | 41                | 40                | 39                | 38                | 37                | 36               | 35                | 34                | ω<br>ω            | 32                | 31                | 30                | 29                | 28                |  |
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|            | 370               | 370              | 341              | 318                | 316               | 251               | 234               | 234               | 197               | 197              | 197               | 197               | 197               | 175               | 175               | 175               | 154               | 154               |  |
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| ALTGUMENTS | US-09-028-934-27  | US-08-729-214-27 | US-09-347-803-16 | US-09-615-192A-389 | US-09-347-803-20  | US-09-149-476-568 | US-09-295-055-3   | US-08-903-801-3   | US-09-228-152-24  | US-08-469-219-24 | US-08-779-379-24  | US-08-467-389-24  | US-08-468-347-24  | US-09-022-765-4   | US-09-183-861-4   | US-08-533-669A-4  | US-09-346-510B-1  | US-08-871-732A-1  |  |
|            | Sequence 27, Appl |                  |                  | _                  | Sequence 20, Appl | Sequence 568, App | Sequence 3, Appli | Sequence 3, Appli | Sequence 24, Appl |                  | Sequence 24, Appl | Sequence 24, Appl | Sequence 24, Appl | Sequence 4, Appli | Sequence 4, Appli | Sequence 4, Appl1 | Sequence 1, Appli | Sequence 1, Appli |  |

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; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-487-810-2
                                                                                                                         APPLICATION NUMBER: US
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
SEQUENCE: 381 amino acid
                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                       Application
                                                                                                                           381 amino acids
Conservative
             11.9%;
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             Score 7; pred. No
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Smith & Reynolds, P.C.

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RESULT 3
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/743,130A
FILING DATE: 01-NOV-1996
CLASSIFICATION: 435
ATTORNEY/AGFANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 39,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: POS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/743,130A
FILING DATE: 01-NOV-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: CANDIDA TYROSYL-TRNA SYNTHETASE
TITLE OF INVENTION: PROTEINS, NUCLEIC ACIDS AND STRAINS COMPRISING SAME
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSE: Hamilton, Brook, Smith & Reynolds, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tent No.
                                                         ATTORNEY/AGENT INFORMATION:
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LENGTH: 409 amino acids
TYPE: amino acid
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NAME: Brook Esg., David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: CP195-12
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      360 KQEKKKK 366
NAME: Brook Esq., David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: CP:
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                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 02173
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Tao, Jianshi
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Gallant, Paul L.
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Pred. No.
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Query Match
Best Local Similarity
Thes 7; Conserv
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US-09-568-102-5
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APPLICANT: Cyr, Devon
APPLICANT: Goerlach, Joern
APPLICANT: Goerlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
CURRENT FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: 09/935,409
PRIOR APPLICATION NUMBER: 09/335,409
PRIOR FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 527
                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James
                                                                                                                                                                                                                                                              Sequence 5
Patent No.
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Matches
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APPLICANT: Ligon, James
APPLICANT: Molhar, Istvan
APPLICANT: Sirkle, Ross
APPLICANT: Cyr, Devon
APPLICANT: Gerlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
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CURRENT FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
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TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (617) 861-9540 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                            7250 SLARAGK 7256
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ses 7; Conserva
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o. 6346404
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Zirkle, Ross
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: SEQ ID NO 5
; LENGTH: 7257
; TYPE: PRT
; ORGANISM: Sorangium cellulosum
US-09-567-969-5
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Best Local Similarity
Thes 7; Conserv
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                                 ; SEQ ID NO 5; LENGTH: 7257; TYPE: PRT; ORGANISM: Sorangium cellulosum US-09-568-480-5
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Matches 7; Conserv
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Best Local
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   Query Match
                                                                                                                   CURRENT APPLICATION NUMBER: US/09/568,480 CURRENT FILING DATE: 2000-05-10 PRIOR APPLICATION NUMBER: 09/335,409 PRIOR FILING DATE: 1999-06-17 NUMBER OF SEQ ID NOS: 30 SOFTWARE: Patentin Ver. 2.0
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CURRENT FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: 09/335,409
PRIOR FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
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APPLICANT: Ligon, James
APPLICANT: Molnar, Istvan
APPLICANT: Zirkle, Ross
APPLICANT: Cyr, Devon
APPLICANT: Goerlach, Joern
APPLICANT: Goerlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
                                                                                                                                                                                                                       APPLICANT: Cyr, Devon
APPLICANT: Goerlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS
FILE REFERENCE: 4-30582A
                                                                                                                                                                                                                                                                                       APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James
APPLICANT: Molnar, Istvan
APPLICANT: Zirkle, Ross
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   Score 7;
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                                                                                               ; SEQ ID NO 5;
LENGTH: 7257
; TYPE: PRT
; ORGANISM: Sorangium cellulosum
US-09-568-472-5
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                                Best Local
Matches
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                                                                                                                                                                            APPLICANT: Cyr, Devon
APPLICANT: Goerlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
CURRENT APPLICATION NUMBER: US/09/568,472
CURRENT FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: 09/335,409
PRIOR APPLICATION NUMBER: 09/335,409
PRIOR FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
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APPLICANT: Goerlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
CURRENT APPLICATION NUMBER: US/09/568,486
CURRENT FILING DATE: 2000-05-10
CURRENT FILING DATE: 2000-05-10
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PRIOR FILING DATE: 1999-06-17
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Zirkle, Ross
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                             11.9%; Score 7; DB ilarity 100.0%; Pred. No. 95 Conservative 0; Mismatches
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100.0%; Pr/
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); Mismatches
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                                                DB 4;
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7250 SLARAGK 7256

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Query Match
Best Local Similarity
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                                                                              RESULT 12
US-09-082-3588-62
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: TYPE: PRT
: ORGANISM: Sorangium cellulosum
US-09-567-899-5
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US-09-567-899-5
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SOFTWARE: PatentIn Ver. 2
SEQ ID NO 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 24, Application US/09082358B Patent No. 6469153 GENERAL INFORMATION:
                                  GENERAL INFORMATION:
                                                   Sequence 62, Application US/09082358B Patent No. 6469153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/567,899
CURRENT FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: 09/335,409
PRIOR FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
SEQ ID NO 5
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                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: GOff, Stephen P.
APPLICANT: Li, Xingquiang
TITLE OF INVENTION: EIP-1, EIP-3 GENES, ENVELOPE-INTERACTING PROTEINS,
TITLE OF INVENTION: EIP-1, and EIP-3
FILE REFERENCE: 0575/54804
CURRENT APPLICATION NUMBER: US/09/082,358B
CURRENT FILING DATE: 1998-05-20
APPLICANT: Goff, Stephen P. APPLICANT: Li, Xingquiang
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TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James
APPLICANT: Molnar, Istva
APPLICANT: Zirkle, Ross
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                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: murine
                                                                                                                                                                                                                                                                                                                          LENGTH: 15
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                                                                                                                                                                  23 EKKKKK 28
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Zirkle, Ross
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                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ilarity 100.0%;
Conservative 0;
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Pred. No.
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Mismatches
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Best Local Similarity
"~+~hes 6; Conserv?
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US-08-851-843A-201
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CURRENT FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 106
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 201,
               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: EIP-1, EIP-3 GENES, ENVELOPE-INTERACTING PROTEINS, TITLE OF INVENTION: EIP-1, and EIP-3 FILE REFERENCE: 0575/54804
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TYPE: PRT
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                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 18-APR-1997
                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
CRASSIFICATION DATA:
PRIOR APPLICATION NUMBER: US 08/846,017
SEQUENCE CHARACTERISTICS:
                                           TELEPHONE: (415) 576-0200
                                                                                                                                                                CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: US 08/724,643
                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 06-MAY-1997
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                                                                                                                         ATTORNEY/AGENT INFORMATION:
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                              TELEPHONE:
                                                                          NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 01
                                                                                                                                                                                                          FILING DATE: 1
CLASSIFICATION:
                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 0 FILING DATE: 25-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                               CLASSIFICATION:
                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                            CLASSIFICATION:
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T: Two Embarcadero Center, 8th Floor
San Francisco
California
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f: Andrews, William H.
INVENTION: No. 6093809el Telomerase
F SEQUENCES: 225
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                              (415)
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                                                                                                                                                                                  APPLICATION NUMBER: US 01 FILING DATE: 09-MAY-1997 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/846,017 FILING DATE: 25-APR-1997 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
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MEDIUM TYPE: Floppy disk
                                                                                                                                 APPLICATION NUMBER: US 08/911,312 FILING DATE: 14-AUG-1997 PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
FILING DATE: 18-APR-
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                                                                             FILING DATE: 14-AUG-
PRIOR APPLICATION DATA:
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CITY: San Francisco
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 01
FILING DATE: 01-OCT-1996
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Similarity 100.0%;
6; Conservative
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                                                                                                   NUMBER: US 08/912,951
14-AUG-1997
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                                                                                                                                                                                                                                                                                                                                                             UMBER: US 08/844,419
18-APR-1997
                                                  14-AUG-1997
MBER: WO PCT/US97/17618
01-OCT-1997
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                                                               US 08/915,503
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b; Pred. No. 7.2
0; Mismatches
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Best Local Similarity
watches 6; Conserve
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; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-974-549A-320
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                                                                                                                                                                                                SOFTWARE: PatentIn Releaction CURRENT APPLICATION NUMBER: US/O FILING DATE: 09-WAY-199 CLASSIFICATION: 536 PRIOR APPLICATION DATA:
                                                                                                                                    CLASSIFICATION: 536
PRIOR APPLICATION DATA:
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LENGTH: 16 amino acids
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REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
              PRIOR APPLICATION DATA:
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                                                                                          CLASSIFICATION:
                                                                                                         APPLICATION NUMBER: US 08/846,017 FILING DATE: 25-APR-1997
                                                                                                                                                                      APPLICATION NUMBER: US 0: FILING DATE: 06-MAY-1997
                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                           APPLICATION NUMBER:
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FENTION: No. 6261836el Telomerase
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Chapman, Karen B.
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                                             18-APR-1997
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US 08/724,643
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REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 01:
TELECOMMUNICATION INFORMATION:
TELECHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
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TOPOLOGY: 11
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es 6; Conserv
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APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: APPLE, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/430,323
FILING DATE: 29-OCT-1999
CLASSIFICATION: <UNknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 2/2)
CORRESPONDENCE ADDRESS:
ADDRESSE: Two Embarcadero Center, 8th Floor
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Andrews, William H.
TITLE OF INVENTION: No. 6309867el Telomerase
NUMBER OF SEQUENCES: 225
                                                                                                                                          APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
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                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/851,843 FILING DATE: 06-MAY-1997
                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/854,050 FILING DATE: 09-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: California
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Harley, Calvin
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Nakamura, Toru
Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thomas R.
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APPLICANT: Marvey, Combined B.
APPLICANT: Goldberg, Robert B.
APPLICANT: The Regents of the University of California
ITILE OF INVENTION: Nucleic Acids That Control Seed and Fruit
ITILE OF INVENTION: Development in Plants
FILE REFERENCE: 023070-086120US
CURRENT APPLICATION NUMBER: US/09/177,249
CURRENT FILING DATE: 1998-10-22
EARLIER APPLICATION NUMBER: US 09/071,838
EARLIER APPLICATION NUMBER: US 09/071,838
EARLIER FILING DATE: 1998-05-01
NUMBER OF SEQ ID NOS: 324
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 189
LENGTH: 29
LENGTH: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Fischer, Robert L.
APPLICANT: Ohad, Nir
APPLICANT: Kiyosue, Tomohiro
APPLICANT: Yadegari, Ramin
APPLICANT: Margossian, Linda
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US-09-227-357-479
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MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 201:
US-09-430-323-201
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CURRENT APPLICATION NUMBER: US/09/227,357
CURRENT FILING DATE: 1999-01-08
EARLIER APPLICATION NUMBER: PCT/US98/13684
EARLIER FILING DATE: 1998-07-07
EARLIER APPLICATION NUMBER: 60/051,926
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,793
EARLIER FILING DATE: 1997-07-08
                                                                                                                                                                                                                                      Sequence 479, Application US/09227357 Patent No. 6342581
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Matches
                                                                                                                                                    APPLICANT: Fischer et al.
TITLE OF INVENTION: 123 Human Secreted Proteins
FILE REFERENCE: PZ010P1
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Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                               48 TFGKKK 53
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hes 6; Conserv
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TYPE: amino acid
STRANDEDNESS: <Unknown>
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100.0%; P1
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100.0%; Pr
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b; Pred. No. 12;
0; Mismatches
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b; Pred. No. 7.2
0; Mismatches
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5. 7.2;
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APPLICATION NUMBER: 60/051,931 FILING DATE: 1997-07-08 FILING DATE: 1997-07-08 APPLICATION NUMBER: 60/052,732

APPLICATION NUMBER: 60/051,929 FILING DATE: 1997-07-08 APPLICATION NUMBER: 60/051,925

1997-07-08

APPLICATION NUMBER: 60/052,803

1997-07-08

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Query Match
Best Local Similarity
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                                                                                             ; ORGANISM: Homo sapiens US-09-227-357-479
                                                                                                                         NUMBER OF SEQ ID NOS: 672
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 479
LENGTH: 51
TYPE: PRT
                                                                                                                                                                                                      EARLIER APPLICATION NUMBER: 60/058,660 EARLIER FILING DATE: 1997-09-12 EARLIER APPLICATION NUMBER: 60/058,661 EARLIER FILING DATE: 1997-09-12
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EARLIER
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 23 EKKKKK 28
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APPLICATION NUMBER: 60/051 916
FILING DATE
                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/
FILING DATE: 1997-09-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/055,950 FILING DATE: 1997-08-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/055,722
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                                                                                                                                                                                                                                                                                                                                     FILING DATE: 1997-08-18
                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/055,954
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
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                                Conservative
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                           10.2%; Score 6; DB (100.0%; Pred. No. 19)
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                                               DB 4;
o. 19;
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                                                           Length 51;
                                Indels
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Query Match
Best Local Similarity
6; Conserve
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US-08-569-749-6
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                                                                                                                                         Sequence 6, Application US/08569749
Patent No. 6187557
GENERAL INFORMATION:
APPLICANT: Rothe, Mike
APPLICANT: Goeddel, David V
APPLICANT: Goeddel, David V
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 55 amino 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/08569749 Patent No. 6187557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Rothe, Mike
APPLICANT: Goeddel, David V
TITLE OF INVENTION: INHIBITORS OF
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: line
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: A-TELECOMMUNICATION INFORMATION: TELEPHONE: (415)781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Brezner, David J.
REGISTRATION NUMBER: 24,774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: San Francisco
STATE: California
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                                                                              STREET: 4 Embarcadero Center, Suite 3400 CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                        22 SLARAG
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CLASSIFICATION: 514
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                                                                COUNTRY:
                                                                                                                              ADDRESSEE:
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                                                                                                                               FLEHR,
                                                                                                                               HOHBACH, TEST, ALBRITTON & HERBERT
                                                                                                                                                                                                                                                                                                                                                                                                                       10.2%; Score 6; 100.0%; Pred. No.
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PCT-US96-12860-5
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Best Local :
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                                                                                                                                                                                                                                             TELEFAX: (415)398-324 INFORMATION FOR SEQ ID NO:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)781-1989
TELEFAX: (415)398-3249
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/12860
FILING DATE: 06 AUG 1996
                             TOPOLOGY: li
                                                                                                                                                                   SEQUENCE CHARACTERISTICS: LENGTH: 55 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION_NUMBER: U.S. Serial Nos. 08/512,946 & 08/569,749
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                                                                                                                                                                                                                                                                                                                       TELEPHONE: (415)781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
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NAME: Brezner, David J.
REGISTRATION NUMBER: 24,
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                                                                                                                                                                                                                                                                                                                                                                                          NAME: Brezner, David J.
REGISTRATION NUMBER: 24,774
REFERENCE/DOCKET NUMBER: A-
                                                                                                    STRANDEDNESS:
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TYPE: amino acid
STRANDEDNESS: single
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SOFTWARE: Patentl
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                                                                                                                                     amino acid
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                                                                                                                                                                                                                                                                                  (415)398-3249
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linear
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PatentIn Release #1.0, Version #1.30
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RESULT 23
US-09-082-358B-43
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                                                                                                            GENERAL INFORMATION:
                                                                                                                            Sequence 43, Application US/09082358B Patent No. 6469153
                                                                                                                                                                                                                                                                                         Matches
                       APPLICANT: Goff, Stephen P.
APPLICANT: Li, Xingquiang
TITLE OF INVENTION: EIP-1, EIP-3 GENES, ENVELOPE-INTERACTING PROTEINS,
TITLE OF INVENTION: EIP-1, and EIP-3
FILE REFERENCE: 0575/54804
                                                                                                                                                                                                                                                                                                                      Query Match
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GENERAL INFORMATION:
CURRENT APPLICATION NUMBER: US/09/082,358B CURRENT FILING DATE: 1998-05-20
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                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 55 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                          22 SLARAG
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STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Brezner, David J
REGISTRATION NUMBER: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/US96/12860 FILING DATE: 06 AUG 1996
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nes 6; Conserv
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STREET: 4 Embarcadero Center,
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100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                      Score 6; Pred. No.
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RESULT 25

US-08-511-485-18

; Sequence 18, Application US/08511485

; Patent No. 5919912
                                                                                                                                 Query Match
Best Local Similarity
"---hes 6; Conserv
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                                                                                                                                                                                                    ; MOLECULE TYPE: protein US-08-971-089-2
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US-08-971-089-2
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Patent No. 6376174
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Pulst, Stefan M.
                                                                                                                                                                                                                                                                                       TELEFAX: (619)535-8949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 57
TYPE: PRT
ORGANISM: murine
                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 63 amino acids
                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/030,987
FILING DATE: 15-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ramos, Robert T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/971,089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Scoles, Daniel R.
TITLE OF INVENTION: NUCLEIC ACID ENCODING
TITLE OF INVENTION: SCHWANNOMIN-BINDING-PROTEINS AND PRODUCTS RELATED THERETO
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: (619)535-9001
                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 9-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 4370 La
CITY: San Diego
STATE: Californi
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nes 6; Conserv
                                                                                        15 EKKKKK 20
                                                                                                                  23 EKKKKK 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
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                                                                                                                                                                                                                                              amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   United States
                                                                                                                                                                                                                                                                                                       (619)535-8949
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                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAMPBELL & FLORES, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Floppy disk
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                                                                                                                                             ; Score 6; DB 4
b; Pred. No. 22;
0; Mismatches
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5. 22;
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                                                                                                                                                                                                                                                                                                                      Patent No. 5919912
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                         Sequence 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/511
FILING DATE: 04-AUG-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 0754
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 68 amino a TYPE: amino acid STRANDEDNESS: not TOPOLOGY: both MOLECULE TYPE: prot
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Re-lease #1.0, Version #1.30
CURRENT APPLICATION DATA:
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APPLICANT: Mackenzie, Alexander E.
APPLICANT: Baird, Stephen
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Ric
STREET: 225 Franklin
                                                                                                                                                                                                                                                                   APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Baird, Stephen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 68 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                      TITLE OF INVENTION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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STATE: MA
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                                                                                                                                     STATE:
                                                                                                                                                   CITY: Boston
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5919912
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100.0%; Pred. No.
1ve 0; Mismatches
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lin Street
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5. 23;
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Query Match
Best Local Similarity
Conserve
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US-09-091-725-51
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; MOLECULE TYPE:
US-08-511-485-19
                                                                                                                                      APPLICATION NUMBER: EP 96200943.7
FILING DATE: 11-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: E. VICTOR DONAHUE
REGISTRATION NUMBER: 35,492
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 141 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 51, Application US/09091725
Patent No. 6329141
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Matches 6; Conserv
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                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95203620.0
FILING DATE: 22-DEC-1995
                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 68 amino acids
TYPE: amino acid
STRANDEDNESS: not relev
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TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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NAME: Clark, Paul T.
RECISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 07540/002001
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21 SLARAG 26
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                                                                                                                            TYPE:
                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/091,725 FILING DATE: 23-DEC-1996 CLASSIFICATION: 435
                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: United ZIP: 20006-1888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Morrison & Foerster llp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Washington
                                                                                                                        amino acid
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              Conservative
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         10.2%; Score 6; DB 4
100.0%; Pred. No. 43;
tive 0; Mismatches
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Pred. No.
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23;
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5. 43;
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; STRANDEDNESS:
; TOPOLOGY: LIN
; MOLECULE TYPE:
US-08-871-732A-1
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US-08-871-732A-1
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                                                                                                 GENERAL INFORMATION:
APPLICANT: O'Brien, Timot
APPLICANT: Wang, Yinxiang
                                                                                                                                                      Sequence 1, Application US/09346510B Patent No. 6281014
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                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                   Query Match
CURRENT APPLICATION NUMBER: US/09/346,510B
CURRENT FILING DATE: 1999-07-01
PRIOR APPLICATION NUMBER: 08/871,732
PRIOR FILING DATE: 1997-06-09
                                                                    TITLE OF INVENTION: FILE REFERENCE: D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: NONE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION UMBER: 29,329
REFERENCE/DOCKET NUMBER: 1-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-682-1213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
NAME: MCGREGOR, MARTIN L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: WORDPERFECT 6.1
CURRENT APPLICATION DATA:
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MEDIUM TYPE: DISKETTE 3.5 INCH 1.44 MB STORAGE
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CORRESPONDENCE ADDRESS:
ADDRESSEE: MARTIN L. MCGREGOR
STREET: 5380 WEST 34TH STREET, #345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: NOVEL SH3 PROTEIN, GENE, CHITITLE OF INVENTION: CELLS, VECTORS AND EXPRESSION PROTEIN, ANTIBODIES AND USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: O'BRIEN, TIMOTHY J. APPLICANT: WANG, YIN
                                                                                                                                                                                                                                                                                                                                 Local Similarity
nes 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/871,732A FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM COMPATIBLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: TEXAS
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                                                                                                                    O'Brien, Timothy J.
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100.0%; P
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%; Pred. No. 46;
0; Mismatches
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                                                                                    DNA and Uses Thereof
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; FEATURE: ; OTHER INFORMATION: amino acid sequence of TADG5 protein US-09-346-510B-1
                                               RESULT 31
US-09-183-861-4
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         Sequence 4, Application US/09183861 Patent No. 6365165 GENERAL INFORMATION:
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Best Local
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                                                                                                                                                    Matches
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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ORGANISM: Homo
                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 22-SEP-1995
CLASSIFICATION: 424
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: CORIXA CORPORATION
TITLE OF INVENTION: THERAPY AND DIAGNOSIS
                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: SEED and BERRY LLP
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                   160 AKRRMQ
                                                                                                                                                   Local Similarity
nes 6; Conserv
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nes 6; Conserv
                                                                                                                          32 AKRRMQ 37
                                                                                                                                                                                                                                                                                                                                         NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                        TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
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GY: linear
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                                                                                                                                                                                                                                                  175 amino acids
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Reed, Steven G.
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Pred. No
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Pred. No.
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RESULT 32
US-09-022-765-4
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Best Local
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/0
EFILING DATE: 12-FEB-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                      APPLICANT: Dillon, Davin C. APPLICANT: Skeiky, Yasir A.W. TITLE OF INVENTION: LEISHMANI
                                                                                                                                                                                                                                                APPLICANT: Reed, Stever APPLICANT: Campos-Neto,
                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                   APPLICANT:
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                                                                                           STREET: 6300 CONTY: Seattle STATE: Washing:
                                                                                                                                                                                                                                                                                                                                                                                         160 AKRRMQ 165
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REGISTRATION NUMBER: 31,392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                            COUNTRY:
                                                                                                                                         ADDRESSEE:
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98104-7092
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Skeiky, Yasir A.W.
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100.0%; Prr
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Pred. No.
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PatentIn Release #1.0,

Version #1.30

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GENERAL INFORMATION:
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Best Local :
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REFERENCE/DOCKET NUMBER: 2101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/225,442
FILING DATE: 08-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0317/43
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                                                           TELEFAX: 212-664-0525 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 175 amino acids
                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 197 amino acid
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CORRESPONDENCE ADDRESS:
           MOLECULE TYPE:
HYPOTHETICAL:
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APPLICATION NUMBER: US
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ANTI-SENSE:
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                                                          TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
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CLASSIFICATION:
                                             TOPOLOGY:
                                                                                                                                                          TELEPHONE:
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New York
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                                                                                        197 amino acids
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ENTION: NOVEL POLYPEPTIDE HAVING FACTOR XA
ENTION: INHIBITORY ACTIVITY
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                                                                                                                                                           212-977-9550
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100.0%; Pr
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Pred. No. 51;
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Best Local Similarity
Watches 6; Conserva
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; LOCATION:
US-08-468-347-24
                                                                                       ; LOCATION: US-08-467-389-24
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US-08-467-389-24
                                  Query Match
Best Local S
Matches 6
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Patent No.
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                                                                                                                                                                                                                                                             TELEFAX: 212-664-0525
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 03
                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/2
FILING DATE: 08-APR-1994
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                                                                                                                            FRAGMENT TYPE: FEATURE:
                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 197 amino acids
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ADDRESSEE: Cooper & Dunham
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Zeelon, Elisha P.
APPLICANT: Werber, Moshe M.
APPLICANT: Levanon, Avigdor
TITLE OF INVENTION: NOVEL POLYPEPTIDE HAVING FACTOR XA
                                                                                                                                                     ANTI-SENSE:
                                                                                                                                                                HYPOTHETICAL:
                                                                                                                                                                               TOPOLOGY: li
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24 KKKKKT 29
                                  Local Similarity
les 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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                                                                                                                                                                                                       STRANDEDNESS:
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                                                                                                                 NAME/KEY:
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o. 5824641
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                                                                                                                                                                                                                     amino acid
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linear
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                                                                                                                                          N-terminal
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                                               Score 6;
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Pred. No.
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Mismatches
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56;
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191 KKKKKT 196

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RESULT 36
US-08-469-219-24
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                                                                                                                                          Sequence 24, Application US/08469219 Patent No. 5863534
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Patent No. 5858970
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INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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ETING DATE: 08 APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0317
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212,977-9550
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MOLECULE TYPE: Pro-
HYPOTHETICAL: NO
HYPOTHETICAL: NO
                                         APPLICANT: Zeelon, I
APPLICANT: Werber, I
APPLICANT: Levanon,
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:
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STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: sir
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Zeelon, Elisia...
Zeelon, Elisia...
Xeelon, Moshe M.
Werber, Moshe M.
Levanon, Avigdor
NVENTION: NOVEL POLYPEPTIDE HAVING FACTOR Xa
NVENTION: INHIBITORY ACTIVITY
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30 Rockefeller Plaza
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Werber, Moshe M.
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1..197
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Pred. No.
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RESULT 37
US-09-228-152-24
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; LOCATION:
US-08-469-219-24
US-09-228-152-24
                                                                                                                         CURRENT APPLICATION NUMBER: US/09/228,152
CURRENT FILING DATE: 1999-01-11
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 24
                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Zeelon, Elisha P.
APPLICANT: Zeelon, Elisha P.
APPLICANT: Werber, Moshe M.
APPLICANT: Levanon, Aviddor
TITLE OF INVENTION: NOVEL POLYPEPTIDE HAVING FACTOR Xa INHIBITORY ACTIVITY
FILE REFERENCE: 43020aya
                                                                                                                                                                                                                                                                                                                                             Patent No.
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INFORMATION FOR SEQ ID NO:
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FILING DATE:
CLASSIFICATION: 435
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/225,442
APPLICATION NUMBER: 08/225,442
AFTING DATE: 08-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0317/43020
         FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Deduced amino OTHER INFORMATION: acid sequence of clone psp65-XaI-13.
                                                       LENGTH: 197
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: 212-977-9550 TELEFAX: 212-664-0525
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CORRESPONDENCE ADDRESS:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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les 6; Conserva
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STRANDEDNESS: single
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30 Rockefeller Plaza
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1..197
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100.0%; Pred. No.
tive 0; Mismatc
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Sequence 3, Application
Patent No. 6232440
GENERAL INFORMATION:
APPLICANT: Hillman,
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                                                                                                RESULT 39
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Best Local Similarity
Matches 6; Conser
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Patent No. 5932712
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APPLICANT: Hillman, Jennif APPLICANT: Corley, Neil C.
                                                                                                                                                                                                                                                                                                                       IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749 REGERENCE/DOCKET NUMBER: PETELECOMMUNICATION INFORMATION: TELEPHONE: 415.855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTEK: L... DOS
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
COMPUTER: US/08/903,801
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatil
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APPLICANT: Shah, Purvi
TITLE OF INVENTION: NEW ANEXIN BINDING PROTEIN
NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                 217 KKKKKT 222
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nes 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
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                                                               Application US/09295055
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                                                                                                                                                                                                                                                                                                                                                                                     234 amino acids
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100.0%; Pred. No.
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Pred. No. 56;
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                                                                           CURRENT APPLICATION NUMBER: US/09/149,476
CURRENT FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER FILING DATE: 1998-03-06
EARLIER APPLICATION NUMBER: 60/040,162
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER APPLICATION NUMBER: 60/038,621
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
                                                                                                                                                                                                                                                                                                                                      RESULT 40
US-09-149-476-568
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US-09-295-055-3
                                                                                                                                                                                                                                                                                                       Sequence 568, App
Patent No. 64205
                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                           APPLICANT: Rosen et al. TITLE OF INVENTION: 186 Human Secreted proteins FILE REFERENCE: PZ002P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                EARLIER
                                                                 EARLIER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: NEW ANEXIN BINDING PROTEIN NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MMEDIAL
LIBRARY: Gen-
TONE: 1514949
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TELEFAX: 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
                                              APPLICATION NUMBER: 60/040,626 FILING DATE: 1997-03-07
               APPLICATION NUMBER: 60/040,334 FILING DATE: 1997-03-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               415-845-4166
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ER APPLICATION NUMBER: 60/056,894
ER FILING DATE: 1997-08-22
LER APPLICATION NUMBER: 60/056,911
IER FILING DATE: 1997-08-22
LER APPLICATION NUMBER: 60/056,636
JER FILING DATE: 1997-08-22
JER APPLICATION NUMBER: 60/056,874
JER APPLICATION NUMBER: 60/056,874
JER APPLICATION NUMBER: 60/056,874 ER FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,910
ER FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,864
ER FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,631
ER FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,845
ER FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/047,595
ER APPLICATION NUMBER: 60/047,595
ER FILING DATE: 1997-05-23
ER APPLICATION NUMBER: 60/047,586
ER FILING DATE: 1997-05-23
ER APPLICATION NUMBER: 60/047,586
ER FILING DATE: 1997-05-23
ER APPLICATION NUMBER: 60/047,596
ER FILING DATE: 1997-05-23
ER APPLICATION NUMBER: 60/043,576
ER FILING DATE: 1997-04-11
ER APPLICATION NUMBER: 60/043,576
ER FILING DATE: 1997-04-11
ER APPLICATION NUMBER: 60/047,596
ER FILING DATE: 1997-04-11 ER FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,630
ER FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,662
ER FILING DATE: 1997-08-22
ER FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,662
ER FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,872
ER FILING DATE: 1997-08-22
ER FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,637
ER APPLICATION NUMBER: 60/056,637
ER APPLICATION NUMBER: 60/056,903
ER APPLICATION NUMBER: 60/056,903
ER APPLICATION NUMBER: 60/056,903
ER FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,879
ER APPLICATION NUMBER: 60/056,879
ER APPLICATION NUMBER: 60/056,879
ER APPLICATION NUMBER: 60/056,879
ER APPLICATION NUMBER: 60/056,889
ER APPLICATION NUMBER: 60/056,889 ER APPLICATION NUMBER: 60/056,886
ER FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,877
ER FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,889
ER FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,893

APPLICATION NUMBER: 60/043,670

1997-04-1

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; SEQ ID NO 20
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Glycine max
US-09-347-803-20
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Best Local Similarity
6; Conserv
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                                                                 Matches
                                                                                                Query Match
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                                                                                                                                                                                                                               APPLICANT: Kinney, Tony
APPLICANT: Orozco, Buddy
TITLE OF INVENTION: Plant Sorbitol Biosynthetic Enzymes
FILE REFERENCE: BB-1176
CURRENT APPLICATION NUMBER: US/09/347,803
CURRENT FILING DATE: 1999-07-02
EARLIER APPLICATION NUMBER: 60/092,952
EARLIER FILING DATE: July 15, 1998
NUMBER OF SEQ ID NOS: 27
                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Famodu, Layo O. APPLICANT: Hitz, Bill
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134 VHGSLA 139
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                                                               Local Similarity tes 6; Conserv
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                              2 VHGSLA 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/056,909
FILING DATE: 1997-08-2
APPLICATION NUMBER: 60/056,875
FILING DATE: 1997-08-22
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FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,887
FILING DATE: 1997-08-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 1997-10-02
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                                                                 Conservative
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100.0%;
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Pred. No.
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Pred. No.
                                                                 Mismatches
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                                                                                DB 4;
o. 82;
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; SEQ ID NO 16
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Zea mays
US-09-347-803-16
                                                                                                                                                                                                                                            APPLICANT: Famodu, Layo O.
APPLICANT: Hitz, Bill
APPLICANT: Kinney, Tony
APPLICANT: COROCO, Buddy
TITLE OF INVENTION: Plant Sorbitol Biosynthetic Enzymes
FILE REFERENCE: BB-1176
CURRENT APPLICATION NUMBER: US/09/347,803
CURRENT FILING DATE: 1999-07-02
EARLIER APPLICATION NUMBER: 60/092,952
EARLIER APPLICATION NUMBER: 60/092,952
EARLIER TILING DATE: July 15, 1998
NUMBER OF SEQ ID NOS: 27
NUMBER OF SEQ ID NOS: 27
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US-09-347-803-16
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US-09-615-192A-389
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 389
LENGTH: 318
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Bloksberg, Leonard
APPLICANT: Havukkala, Ilka
                                                                                       Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 16, Application US/09347803 Patent No. 6274379
                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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Patent No. 641071
                                                                      Matches
                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/615,192A CURRENT FILING DATE: 2000-07-12 PRIOR APPLICATION NUMBER: US 08/975,316 PRIOR FILING DATE: 1997-11-21 PRIOR APPLICATION NUMBER: US 08/713,000 PRIOR FILING DATE: 1996-09-11 PRIOR APPLICATION NUMBER: US 09/169,789 PRIOR FILING DATE: 1998-10-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Materials and Methods for the TITLE OF INVENTION: Modification of Plant Lignin Content FILE REFERENCE: 11000.1003c4U
                                                                                                                                                                                                                                SOFTWARE: Microsoft Office 97
126 VHGSLA 131
                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92 GPNANS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
nes 6; Conser
                  2 VHGSLA 7
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                                                                      Conservative
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                                                                                     10.2%; Score 6; I
100.0%; Pred. No.
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100.0%; Pred. No.
                                                                  0;
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                                                                      Mismatches
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                                                                                                       Length 341;
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RESULT 44 US-08-729-214-27 : Sequence 27, Application US/08729214 ; Patent No. 5817502

GENERAL INFORMATION:

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; MOLECULE TYPE: protein US-08-729-214-27
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US-09-028-934-27
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: van Pee, Karl-Heinz
APPLICANT: Kirner, Sabine
TITLE OF INVENTION: Genes for the synthesis of
TITLE OF INVENTION: antipathogenic substances
NUMBER OF SEQUENCES: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/729,214
FILING DATE: TBA
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ADDRESSEE: Ciba-Geigy Corporation
STREET: 520 White Plains Road
                                                                                                                                                    TITLE OF INVENTION: Pyrrolnitrin Biosynthesis Genes and TITLE OF INVENTION: Thereof NUMBER OF SEQUENCES: 37
                                                                                                                                                                                                                                                                                        APPLICANT: Ligon, James M
APPLICANT: Hill, Dwight S
APPLICANT: Lam, Steven T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
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NAME: Medgs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Ligon, James M.
APPLICANT: Hill, Dwight Steven
APPLICANT: Ryals, John Andrew
APPLICANT: Hammer, Phillip E.
                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                 APPLICANT:
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                        APPLICANT: Hammer, Philip E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          214 SLARAG 219
                                                  STREET: 3054 Cornwall1s Road
CITY: Research Triangle Park
STATE: NC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 10.2%; Score 6; DB 2; Local Similarity 100.0%; Pred. No. 94; les 6; Conservative n. wirming.
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TYPE: amino acid
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CITY: Tarrytown
STATE: NY
                  COUNTRY: UZIP: 27709
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                                                                                                                  ADDRESSEE:
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Kirner, Sabine
Young, Thomas R.
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                                                                                                                                                                                                                                                                                                           Ligon, James M.
Hill, Dwight S.
                                                                                                             No. 6117670artis Corporation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 370;
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Search completed: February
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Best Local Similarity
"---hes 6; Conserv?
                                                                                                                                                                                                    ; TOPOLOGY: linear; MOLECULE TYPE: protein US-09-028-934-27
                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/729,214
APPLICATION DATA: 09-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/258,261
FILING DATE: 08-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Meligs, J. Timochy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: GGC1506/CI
TELEPHONE: 919-541-8587
                                                                                                                                                                                                                                                              TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 370 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                  214 SLARAG 219
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Maximum DB
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seq length: 2000000000
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Copyright (c) 1993 - 2003 Compugen Ltd.
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| mays protein<br>an seb4B prote<br>an seb4D prote<br>bidopsis thali<br>el human secre | mays promays promays problidopsis bidopsis promays pro | Peptide #2046 enco Human poptide enco Human polypeptide Arabidopsis thalia Arabidopsis thalia Zea mays protein f Zea mays protein f Zea mays protein f Arabidopsis thalia Arabidopsis thalia   | uman di<br>uman di<br>#2100<br>#2131<br>#2034<br>rain ex<br>one mar<br>#2054    |

## ALIGNMENTS

AAR48204 RESULT 1

Rattus norvegicus WPI; 1994-031824/04. (FARH ) HOECHST JAPAN LTD 05-JUN-1992; 05-JUN-1992; 21-DEC-1993. JP05339287-A. Cell growth agent; wound; bone disease; treatment; treating; agent. Heparin-binding protein. 12-JUL-1994 (first entry) AAR48204; AAR48204 standard; protein; 59 AA 92JP-0145125 92JP-0145125

The sequence is that of a heparin binding-protein which is useful as a cell growth agent and in the treatment of wounds and bone disease.

Claim 1; Page 3; 4pp; Japanese

New heparin-binding protein - used as treatment of wounds and bone disease

ø cell

growth agent

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RESULT 2
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                                                                                                                                                                        Sequences AAW95381-389 represent antimicrobial peptide fragments derived from ubiquicidine. Ubiquicidine or optionally modified peptide fragments of ubiquicidine, may be used for the treatment, diagnosis, or prophylaxis of infections in humans and animals. In particular the products and methods are directed against microbial infections caused by pathogenic Gram-positive Staphylococcus aureus, including antibiotic resistant strains, Listeria monocytogenes, and Gram-negative antibiotic resistant Klebsiella pneumoniae, E. coli, enterococci, and Salmonella typhinuriom bacteria, micro-organisms difficult to treat such as Mycobacterium avium and M. fortuitum, fungi such as Candida albicans, Cryptococcus neoformans, and Aspergillus fumigatis, viruses, in particular enveloped viruses, and parasites such as Trypanosoma cruzi ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ubiquicidine; treatment; diagnosis; prophylaxis; infection; microbial; pathogenic; Gram-positive bacteria; antimicrobial; Staphylococcus aureus; Listeria monocytogenes; Gram-negative; Klebsiella pneumoniae; E. coli; enterococcus; Salmonella typhinuriom; Mycobacterium avium; M. fortuitum; fungus; Candida albicans; Cryptococcus neoformans; Aspergillus fumigatis; virus; parasite; Trypanosoma cruzi; Taxoplasma gondii.
                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW95381 standard; peptide;
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                         100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          English
                            .08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59
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Pred. No.
                            Score 59;
Pred. No.
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                         1.9e-54;
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                                                     DB 20;
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                                               Length
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             CC ABPA 328) and to cDNAs encoding them (ABC 41131-ABC 5305), and also CC encompasses polypeptides 90% identical and polynucleotides 95% identical CC to the sequences of the invention. The invention additionally relates to CC recombinant vectors and host cells comprising human ovarian antigen CC polynucleotides, antibodies against human ovarian antigens, and the use CC of ovarian antigen polynucleotides and polypeptides in diagnosing, CC treating, prognosing or preventing various ovary and/or breast-related CC metastratic tumours of ovarian or breast origin, reproductive system CC disorders (e.g., infertility, disorders of pregnancy, anovulation, CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine CC disorders, infections (e.g., chamydia, HIV, toxoplasmosis, and toxic composities, infections (e.g., congenital and acquired conditions include ovarian cysts, and dysmenorrhoea), endocrine CC disorders, infections (e.g., congenital and acquired conditions (e.g., mastitis, opphoritis and confirmations), inflammatory conditions (e.g., mastitis, opphoritis and confirmation of infections (e.g., anaemia), cardiovascular disorders. Ovarian antigen polypeptides and confirmation of infections of the polynucleotides may also be used in screening for compounds which confirmation of infinite and in forested mapping, in the condition of infinite and in forested mapping, in the confirmation of infinite and in forested mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour; ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; pCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection; inflammatory condition; inmune disorder; blood disorder; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antibody preparation; cytostatic; immunomodulatory; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and neurological diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention ABP43228) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neurological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-147878/19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-JUN-2000; 2000US-209467P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABP42408;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABP42408 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ovarian antigen HOCMY79,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABQ55485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID No 3540; 2922pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                           relates to 2175 novel human ovarian antigens (ABP41054-to cDNAs encoding them (ABQ54131-ABQ56305), and also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gynaecological;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       reproductive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polypeptides may be used as food additives or to prepare antibodies useful in disease diagnosis, drug targeting and phenotyping. The present sequence represents a human ovarian antigen of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diagnosis; cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antiviral; antidiabetic; antiarthritic; antiviral; antidifferamentory; antityroid; antialtergic; antibacterial; cardiant; dermatological; neuroprotective; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic; antianglogenic; gene therapy; inflammation; immune disorder; haematopoletic cell disorder; autoimmune disorder; allergic reaction; graft versus host disease; organ rejection;
                                                                                                             AAC77607 to AAC78448 encode the human cancer associated proteins given in AAB43398 to AAB44239. The proteins can have activities based on the tissues and cells the genes are expressed in Example of activities include: cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antirheumatic; antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human cancer associated
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                           antiliflammatory; antilhyroid; antilallergic; antibacterial; antiviral; dermatological; neuroprotective; cardiant; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic and antiangiogenic. The polynucleotides and polypeptides can be used for preventing, treating or amellorating medical conditions and diagnosing pathological conditions.
                                                                                                                                                                                                                Claim 11; Page 1568-1569; 2352pp; English.
                                                                                                                                                                                                                                                 Novel isolated nucleic useful for treating or
                                                                                                                                                                                                                                                                                                                                                                                                                                                08-MAR-2000; 2000WO-US05882
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                 Polynucleotides, polypeptides,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   haemostatic;
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                                                                                                                                                                                                                                                                                                                   2000-587533/55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer associated gene; cancer antigen; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . Similarity
59; Consert
                                                                                                                                                                                                                                                                                                                                                  Ruben
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                thrombolytic;
disease; drug
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                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0124270
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                                                                                                                                                                                                                                                              acids comprising sequences encoding peptides
                                                                                                                                                                                                                                               diagnosing
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   be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cardiovascular disorder; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  screening
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Pred. No.
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                  agonists and
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                  antagonists from
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by activating
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                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or inhibiting the proliferation, differentiation or mobilisation of immune cells, to treat disorders of haematopoietic cells, autoimmune disorders, allergic reactions, graft versus host disease and organ rejection, modulate haemostatic or thrombolytic activity, modulate inflammation, cancers, cardiovascular disorders, neurological disease and bacterial or viral infections. The peptides, nucleotides, antibodies, agonists and antagonists may be also be used in drug screens. AAC78449 to AAC78457 and AAB44240 represent sequences used in the exemplification of
                                                                                                                                                                                                                                                        This is the sequence of a long term potentiation inducing peptide isolated from mice brains by centifugation, extraction, dialysis, reverse phase HPLC and gel filtration chromatography (Sephadex C-25). The peptide is useful for diagnosis and treatment of senile dementia e.g. cerebrovascular or Alzheimer's dementias.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A long-term potentiation inducing peptide and treatment of senile dementia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Long
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SOSE-) SOSEI
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                           KVHGSLARAGKVRGQTPKVAKQEKKKKKTGRAKRRMQYNRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   term potentiation inducing peptide; mouse; brain; senile
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KVHGSLARAGKVRGQTPKVAKQEKKKKKTGRAKRRMQYNRR
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                                                                                                     41;
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                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94JP-0336143
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                                                                                                                                                                                                                                                                                                                                                                                                                 7pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alzheimer's disease
                                                                                                                          69.5%;
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                                                                                                                          Score 41;
Pred. No.
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Pred. No.
                                                                                                     Mismatches
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. 4.7e-54;
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1.1e-35;

    useful for

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41
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                                                                                                     Gaps
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RESULT 6 ABG27228

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ABG27228 standard; Protein; 108

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RESULT 7
ABG27519
ID ABG2
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AC ABG2
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CC specification, but was obtained in electronic format directly from WIPO at firm with funithened and references of the sequence in the printed content of the content o
                                                                                                                                                                                                                                           Matches
                ABG27519;
                                                  ABG27519 standard;
                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAS91415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-639362/73
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23-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel human diagnostic protein #27219.
                                                                                                                                                          69
                                                                                                                                                                     20 AKQEKKKKTGRAKRRMQYNRRFVNVVPTTFGKKKGDNAN 58
                                                                                                                                                                                                                                                                                                                                                         ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                  AKQEKKKKKTGRAKRRMQYNRRFVNVVPTFGKKKGPNAN
                                                                                                                                                                                                                                           39;
                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                         108
                                                                                                                                                                                                                                        Conservative
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2000US-0649167.
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                                                                                                                                                                                                                                                                                                                         AA,
                                                Protein; 108
                                                                                                                                                                                                                                                       66.1%;
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Pred. No.
                                                AA
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3.2e-33;
thes 0;
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                                                                                                 RESULT 8
AAO08731
DXXX ID
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06-NOV-2001 AA008731;

(first entry)

AAO08731 standard;

Protein; 40

B

69

20 AKQEKKKKTGRAKRRMQYNRREVNVVPTFGKKKGDNAN

58

AKQEKKKKTGRAKRRMQYNRRFVNVVPTFGKKKGPNAN 10

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The invention relates to isolated polynucleotide (I) and C polymeride (II) sequences. (I) is useful as hybridisation probes, CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques (C iristore normal activity of (II) or to treat disease states involving CC (II). (II) is useful for generating antibodies against it, detecting or guantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical C imaging of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. CC the polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations CC responsible for genetic disorders or other traits to assess biodiversity and products dependent on DNA and CC amino acid sequences. ABG00010-ABG30377 represent novel human CC diagnostic amino acid sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed CC specification, but was obtained in electronic format directly from WIPO cat first patent did not appear in the printed CC at first patent and products dependent on the printed CC at first patent and products dependent on the printed CC at first patent and products dependent on the printed CC at first patent did not appear in the printed CC at first patent did not appear in the printed CC at first patent did not appear in the printed CC at first patent did not appear in the printed CC at first patent did not appear in the printed CC at first patent did not appear in the printed CC at first patent did not appear in the printed CC at first patent did not appear in the printed CC at first patent did not appear in the printed CCC at first patent did
            Matches
                                    Best
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                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 20; SEQ ID No 57878; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drmanac RT,
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23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAR-2001; 2001WO-US08631.
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       Local Similarity 100 nes 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2001-639362/73.
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                                                                                                      108 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                             66.1%;
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    Score 39; DB; Pred. No. 3.2
       0;
                        DB 22;
3.2e-33;
    0
                                                   Length 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mutations
    0,
Gaps
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RESULT 9
AAG75965
ID AAG7
XX
AC AAG7
XX
DT 03-S
XX
DE Huma
XX
KW Huma
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KW Huma
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KW Homc
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 20; SEQ ID NO 22623; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-FEB-2000; 2000US-0515126.
18-MAY-2000; 2000US-0577409.
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                                                                                                                                                                                                     03-SEP-2001
                                                                                                                                                                                                                                                                                                 AAG75965 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immuni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAI88662.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-FEB-2001; 2001WO-US04927.
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                                                                                                      Human;
                                                                                                                                                Human colon cancer antigen protein SEQ ID NO:6729
                                                                                                                                                                                                                                                       AAG75965;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        treatment of cancer, leukaemia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HYSE-) HYSEQ INC
                       Homo sapiens
                                                                         colorectal carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            23 EKKKKKTGRAKRRMQYNRRFVNVVPTFGKKKGPNANS 59
                                                                                                                                                                                                                                                                                                                                                                                                                                    4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                    EKKKKKTGRAKRRMQYNRRFVNVVPTFGKKKGPNANS
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                                                                                              colon cancer; colon cancer antigen; diagnosis;
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37; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62.7%;
                                                                            chromosome 11.
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Pred. No. 1.7
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 22;
1.7e-31;
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                                                                                                 detection;
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RESULT 10
AAG01569
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent sequences used in the exemplification of the present invention.

N.B. Pages 566 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027 to 1052, 7921 and 7922.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-235357/24.
N-PSDB; AAH35370.
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03-NOV-1999;
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                                                                                                Homo sapiens
                                                                                                                                                                        Human secreted
                                                                                                                                                                                                    06-OCT-2000
                                                                                                                                                                                                                                   AAG01569
                                                                                                                                                                                                                                                              AAG01569 standard; Protein; 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                    106 KVHGSLARAGKVRGQTPKVAKQEKKKKKTGRAKRRMQ 142
                                                                                                                                                                                                                                                                                                                                                    1 KVHGSLARAGKVRGQTPKVAKQEKKKKKTGRAKRRMQ
                                                                                                                             therapy; chromosome mapping.
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                                                                                                                                                                                                                                                                                                                                                                                            l Similarity
37; Conserv
                                                                                                                                            EST;
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99US-0163280.
                                                                                                                                                                      protein, SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                           62.7%; Score 37; 100.0%; Pred. No.
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                                                                                                                                           sequence tag; secreted protein; cDNA isolation;
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5.7e-31;
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21-FEB-2000; 2000EP-0200610

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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; vaccination; gene therapy; nutritional supplement; stem cell proliferation; haematopoiesis; nerve tissue regeneration; immune suppression; immune stimulation; anti-inflammatory; leukaemi
        Nucleic acids encoding a range of human vaccination, testing and therapy -
                                                                                                                                                                                                                                                                                                                                                                                       18-APR-2000;
26-JAN-2001;
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                                                                                                                                     WPI; 2001-611725/70.
                                                                                                                                                                                                                                                                                                     (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel human secreted protein #1363.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU30872 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dumas Milne Edwards
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2001US-0770160
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Pred. No.
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8.6e-26
                                               polypeptides,
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Matches 32
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                                                                                                                              Claim
                                                                                                                                                                                                               New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                    N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAR-2000; 2000US-0540217
23-AUG-2000; 2000US-0649167
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                                                                                                                                                                                            biodiversity
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food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HYSE-) HYSEQ INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72 EKKKKKTGRAKRRMQYNRRFVNVVPTFGKKKG
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100.0%; Pr
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Pred. No.
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1.9e-25;
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes polymerase chain reaction (PCR) primers, oligomers, and for chrome polymerase chain reaction (PCR) primers, oligomers, and for chrome polymerase chain reaction (PCR) primers, oligomers, and for chrome polymerase chain reaction (PCR) primers, oligomers, and for chrome polymerase chain reaction (PCR) primers, oligomers, and for chrome polymerase chain reaction (PCR) primers, oligomers, and for chrome polymerase chain reaction (PCR) primers, oligomers, and for chrome polymerase chain reaction (PCR) primers, oligomers, and for chrome polymerase chain reaction (PCR) primers, oligomers, and for chrome polymerase chain reaction (PCR) primers, oligomers, and for chrome polymerase chain reaction (PCR) primers, oligomers, and for chrome polymerase chain reaction (PCR) primers, oligomers, and for chrome polymerase chain reaction (PCR) primers, oligomers, and for chrome polymerase chain reaction (PCR) primers, oligomers, and for chrome polymerase chain reaction (PCR) primers, oligomers, and primers (PCR) prime

chromosome

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RESULT 13
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CC Note: The sequence data for this patent did not appear in the printed cast efficient on the printed of the printed of the content of the printed of the pr
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Best Local (
The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags
                                                                                                                                                                                                                                                                                                   New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABG27520;
                                                                                                                                                                                                                                         Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drmanac RT, Liu C,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; chromosome mapping; gene mapping; gene therapy; forensic food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABG27520 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HYSE-) HYSEQ INC.
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23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-OCT-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2001-639362/73.
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2000US-0649167
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                                                                                                                                                                                                                             ID No 57879; 103pp;
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Pred. No.
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4.9e-25;
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RESULT 14
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XW Human
XW Human
XW Human
XW Hopel
QX Homo
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CC Note: The sequence data for this patent did not appear in the printed as for the invention.
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26 - MAY - 2000;
30 - JUN - 2000;
03 - AUG - 2000;
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27-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide #2100 encoded by breast cell single exon nucleic acid probe.
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                                                                                                                                                                                                                                                                                                                  2001-496933/54.
                                                                                                                                                                                                                                                                                                                                                                           SG,
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                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULAR DYNAMICS INC
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2000US-0236359
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                                                                                                                                                                                                                                                                                                                                                                           Chen W,
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Pred. No.
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7e-25;
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The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids

New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes -

Claim

IJ

NO 12417;

327pp + sequence

listing;

English.

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ABB34625
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CC bound to each probe of the microarray. The probes are useful for
CC verifying the expression of regions of genomic DNA predicted to
CC encode proteins. They are useful for gene discovery, and for
CC determining predisposition and/or prognosing breast disease. Gene
CC expression analysis is useful for assessing the toxicity of chemical
CC agents on cells. The microarray of this invention presents a far greater
CC diversity of probes for measuring gene expression, with far less bias
CC than expressed sequence tag microarrays. The method is suitable for
CC rapid production of functional information from genomic sequence. The
CC probe of the invention.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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Matches
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the
                                                                                                                                                 Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver -
                                                                                                                                                                                                                                                                                                                                                                                                          30-JAN-2001;
                                                                                                                                                                                                                                                         (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                      27-SEP-2000;
                                                                                                                                                                                                                                                                                                                    21-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200157277-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; foetal liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB34625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB34625 standard; Peptide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ٢
                                                                                                                                                                                                                             SG,
                                                                                                                                                                                                 2001-483447/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KVHGSLARAGKVRGQTPKVAKQEKKKKK 28
                                                                                                                      27; SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KVHGSLARAGKVRGQTPKVAKQEKKKKK 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #2131
                                                                                                                                                                                                                             Hanzel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118 AA;
                                                                                                                                                                                                                                                                                  2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0234687.
2000US-0236359.
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                                                                                                                        IJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           encoded by human
                                                                                                                   NO 27260; 639pp + sequence listing;
                                                                                                                                                                                                                            DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene
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100.0%;
                                                                                                                                                                                                                            Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              expression;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 28;
Pred. No.
                                                                                                                                                                                                                            Rank DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           foetal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single exon nucleic acid probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       liver single exon probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 22;
1.3e-21;
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                                                                                                                   English
                                             from human
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RESULT 16
ABB20035
ABB20037
AC ABB20
AC AC ABB20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                         The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart (see ABA21355-ABA41305). The present sequence is a protein encoded by one succession. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fire wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
  Sequence
                                                                                                                                                                                                                                                                                                                                                                                 Claim 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Single
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04-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             congenital heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; gene expression; cardiovascular disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABB20035;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  hearts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein #2034 encoded by probe for measuring heart cell gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 KVHGSLARAGKVRGQTPKVAKQEKKKKK 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2001-488899/53
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                                                                                                                                                                                                                                                                                                                                                                                                                                     exon nucleic acid probes for analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULAR DYNAMICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                         SEQ ID No 21805; 530pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            118
     118
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2000US-0207456.
2000US-068408.
2000US-0632366.
2000US-0234687.
2000US-0234685.
2000US-02346359.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47.5%;
100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               heart; microarray; vas
hypertension; cardiac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Σ
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rank DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28;
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vascular system;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
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                                                                                                                                                                                                                                                                                                   (see
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Query Match Best Local S Matches 28

Similarity

47.5%;

Score 28; Pred. No.

DB 22; 1.3e-21;

Length 118;

Conservative

0;

Mismatches

0

Indels

0;

Gaps

0

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AAM554117
AAM554117
AAM55117
AAM55
AC A
RESULT 18
AAM67811
ID AAM67
XX
AC AAM67
XX
DT 06-NC
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                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                   Matches
                                                                         AAM67811
                                                                                                                                                                                                                                                                                                                                                                                     brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
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 06-NOV-2001
                                     AAM67811;
                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-483446/52
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27-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM55415 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 4;
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                                                                                                                                                                         56
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                                                                                                                                                                       KVHGSLARAGKVRGQTPKVAKQEKKKKK 83
                                                                                                                                                                                             KVHGSLARAGKVRGQTPKVAKQEKKKKK 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KVHGSLARAGKVRGQTPKVAKQEKKKKK 28
                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULAR DYNAMICS INC
                                                                         standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hanzel
                                                                                                                                                                                                                                                                                                                                                                   of the invention.
                                                                                                                                                                                                                                                                                                                                 118 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
                                                                                                                                                                                                                                                     Conservative
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(first entry)
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                                                                           Protein;
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                                                                                                                                                                                                                                                                   47.5%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27520; 650pp + Sequence Listing; English.
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                                                                           118
                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                     Score 28;
Pred. No.
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                                                                                                                                                                                                                                                   Mismatches
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1.3e-2
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RESULT 19
AAM15620
ID AAM15
XX AAM15
XX 12-OC
XX 12-OC
XX Probe
XX Probe
KW CCTV1
XX CCTV1
XX HOMO
OS HOMO
XX WO200
XX W0200
XX W03-AC
PD 09-AC
XX 30-JE
PR 04-FE
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Best Local S
Matches 28
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancer such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention.
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                                30-JAN-2001;
                                                                    09-AUG-2001
                                                                                                    WO200157278-A2
                                                                                                                                      Homo sapiens.
                                                                                                                                                                        cervical
                                                                                                                                                                                      Probe; human; microarray; gene expression; cervical epithelial cell;
                                                                                                                                                                                                                        Peptide #2054 encoded by probe for measuring cervical gene expression
                                                                                                                                                                                                                                                            12-OCT-2001
                                                                                                                                                                                                                                                                                              AAM15620;
                                                                                                                                                                                                                                                                                                                                AAM15620 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human genome-derived single exon nucleic acid probes useful analyzing gene expression in human bone marrow - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-OCT-2000;
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2000US-0207456
2000US-0608408
2000US-0632366
2000US-0234687
2000US-0236359
                                  2001WO-US00670
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1.3e-
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04-FEB-2000; 2000US-0180312

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RESULT 20
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03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Note: The sequence data for this patent did not form specification, but was obtained in electronic format at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200157272-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genetic disorder.
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                                   SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sapiens
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zing gene expression in
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2000US-0207456.
2000US-0608408.
2000US-0632366.
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2000US-0608408.
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                                   DK,
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                                   Chen
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n human cervical epithelial cell:
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Pred. No.
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                                   Rank DR;
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1.3e-21;
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RESULT 2
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26 - MAY - 2000;
30 - JUN - 2000;
03 - AUG - 2000;
The present invention relates to novel single exon nucleic acid probes (see AAI00010-AAI10067). The present sequence is a peptide encoded by such probe. The probes are useful for measuring human gene expression a human breast sample, where the probe hybridises at high stringency t nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to single exon nucleic acid probes (SENP: see AAI31315-AAI57546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
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27-SEP-2000;
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                                                                                                                                                                                                                                                                                                      2001-476286/51.
                                                                                                                                                                                                                                                                                                                                                   SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KVHGSLARAGKVRGQTPKVAKQEKKKKK 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001-488897/53
                                                                                                                                                                                        27;
                                                                                                                                                                                                                                     single exon nucleic
human breast -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human;
                                                                                                                                                                                                                                                                                                                                                                                               MOLECULAR DYNAMICS INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard; Protein;
                                                                                                                                                                                        SEQ ID No 12104; 322pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID No 28387; 654pp; English
                                                                                                                                                                                                                                                                                                                                                   Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                            2000GB-0024263
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100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disease; breast
proliferative h
                                                                                                                                                                                                                                                                                                                                                   Chen
                                                                                                                                                                                                                                                          acid
                                                                                                                                                                                                                                                                                                                                                   ε
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 28; DB; Pred. No. 1.3
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               exon nucleic ac
n human placenta
                                                                                                                                                                                                                                                       probe used
                                                                                                                                                                                                                                                                                                                                                   Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for measuring
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A
                                                                                                                                                                                                                                                                                                                                                   DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cancer; developments disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 22;
1.3e-21
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nta –
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                                                                                                                                                                                                                                                       measuring gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 118;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disorder;
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diagnosing, gruch human breast, F

polygenic

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ARESULT 2:
ARE 37354
ID ARG:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04 - FEB - 2000;
26 - MAY - 2000;
30 - JUN - 2000;
03 - AUG - 2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease; Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histiccytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; primary ciliary dyskinesis; pulmonary hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  breast disease and non-carcinoma tumours.

Note: The sequence data for this patent did not form specification, but was obtained in electronic format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    aetiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative
                                                                              The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one 12614 nucleic acid sequences mentioned in the specification, or their complements or the 1287 open reading frames derived from the 12614 nucleic acid sequences mentioned in the specification, or their complements or the 1287 open reading frames derived from the 12614 nucleic acid sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-JAN-2001;
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                                                             probes.
                                                                                                                                                                                                                                                              Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                          Spatially-addressable set of single exon nucleic acid probes, used
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            SG,
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                                                                                                                                                                                                                                                           27; SEQ
Also included are a microarray comprising the novel set of
the novel set of probes which hybridise at high stringency to a
acid expressed in the human lung; measuring gene expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULAR DYNAMICS
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2000US-236359P.
2000GB-0024263.
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2000US-0608408.
2000US-0632366.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                               expression
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                                                                                                                                                                                                                                                           ID No 27019;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47.5%;
100.0%;
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                                                                                                                                                                                                                                                        634pp; English.
                                                                                                                                                                                                                                                                                                                  human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                             lung samples
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CC mRNA, and (b) measuring the label detectably bound to each probe of cc (a) algorithmically predicting at least one exon from genomic sequences cc (a) algorithmically predicting at least one exon from genomic sequences cc of the eukaryote; and (b) detecting specific hybridisation of detectably cc labeled nucleic acids from eukaryote lung mRNA, to a single exon probe, cc having a fragment identical to the predicted exon, the probe is included cc in the above mentioned microarray; assigning exons to a single exon probe, comprising (a) identifying exons from genomic sequence by the method cc above and (b) measuring the expression of each of the exon in several cc itssues and/or cell types using hybridisation to a single exon cc microarrays having a probe with the exon, where a common pattern of ce expression of the exons in the tissues and/or cell types indicates that the exons should be assigned to a single gene, a peptide comprising one of 12011 sequences, mentioned in the specification, or encoded by the cc probes/open reading frames (ORF). The probes are used for gene cc expression analysis, and for identifying exons in a gene, particularly using human lung derived mRNA and for the study of lung diseases (CCOPD), interstitial lung disease (ILD), familial idiopathic pulmonary cc fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease, cc unimonary disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary disease. The prevented to a peptide/protein contended by a single exon probe of the invention form particular of the printed specification, but was obtained in electronic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sample derived from human lung, comprising (a) contacting a collection of detectably labeled nucleic acids derived
                                                                                                                                                                                                                                                                    Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                   (HYSE-)
                                                                    28-FEB-2000;
18-MAY-2000;
                                                                                                                    26-FEB-2001; 2001WO-US04927.
                                                                                                                                                       07-SEP-2001.
                                                                                                                                                                                     WO200164835-A2
                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                        nervous
                                                                                                                                                                                                                                                                                                                                         Human polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                                            AAO07113;
                                                                                                                                                                                                                                                                                                                                                                                                                                             AAO07113 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of the printed specification, but was obtained format directly from WIPO at
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28; Conserv
                                   HYSEQ INC
                                                                                                                                                                                                                                                      system disorders;
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                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                  2000US-0515126
2000US-0577409
                                                                                                                                                                                                                                                                                                                                         SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47.5%;
                                                                                                                                                                                                                                                      arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                             35
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                                                                                                                                                                                                                                                                                                                                           21005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 28;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                             ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                        inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.3e-21;
hes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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| 05-AUG-1 | 04-2   | 03-A     | 02-2       | 02-4   | 28-ม   | 27-1    | 27-J   | 26-ม   | 23-ป   | 23-J   | 23-    | 22-J         | 22-1   | ٠،<br>د-د | 7.17   | 21-J   | 21-J   | 20-J   | 20-J   | 20-1    | 10-1<br>10-1 | 1 L    | 19-0   | 19-0   | 19-0   | 16-J   | 16-5   | 1 5    | 14-    | 1 L    | 12 - J | ָר בּי<br>בּי | 20-1   | 06-J   | 02-J   | 01-J   | J-10   | 30-J   | 29-J   | 28-1        | 2 4 5                           | 2 | 22-J   | 21-ປ      | 18-ປ      | 18-1     | 18-J   | 18-J   | 18-J      | 18-3     | 18-J   | 18-J   | 18-J      | 18-J   | 17-J      | 16-7      | 14-0   | 10-J   | 10-J   | r-80   | 07-1      | 04.5   | , |
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| e 22;    |        |          |            |        |        |         |        |        |        |        |        |              |        |           |        |        |        |        |        |         |              |        |        |        |        |        |        |        |        |        |        |               |        |        |        |        |        |        |        |             |                                 |   |        |           |           |          |        |        |           |          |        |        |           |        |           |           |        |        |        |        |           |        |   |
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| th 62;   |        |          |            |        |        |         |        |        |        |        |        |              |        |           |        |        |        |        |        |         |              |        |        |        |        |        |        |        |        |        |        |               |        |        |        |        |        |        |        |             |                                 |   |        |           |           |          |        |        |           |          |        |        |           |        |           |           |        |        |        |        |           |        |   |
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| 99US-0137724. 99US-0138094. 99US-0138540. 99US-0138847. 99US-0139119.             | 990S-0137522.<br>990S-0137528.<br>990S-0137502. | 99US-0136021.<br>99US-0136392.<br>99US-0136392. | 99US-0135353<br>99US-0135629. | 99US-0134941.<br>99US-0135124 | 99US-0134370.<br>99US-0134768 | 99US-0134219.<br>99US-0134221 | 99US-0134256.<br>99US-0134218             | 99US-0132487.<br>99US-0132867. | 99US-0132485. | 99US-0132407.<br>99US-0132407.<br>99US-0132484 | 99US-0131449. | 99US-0130510.  | 99US-0130077.<br>99US-0130449. | 99US-0128714.<br>99US-0129845. | 9905-012/462.            | 99US-0126785. | 99US-0125788.<br>99US-0126264. | 99US-0123180.<br>99US-0123548. | 99us-0121825.            | 2000EP-0301439. |              |                  | p. mays.        | Orn.          | signal transduction     | ein fragment SEQ ID NO: 41466. | (first entry)            |                            | standard; Protein; 62 AA. |                          |            | KVHGSI-ARAGKVRGOTEKVAKO 22<br>          |  |
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RESULT 32
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|---|--|----------------|----------------|---------|---------------------------|----------------|-------|--------------|-------------------|------------|-------|-------|------------|-------|----------------|-------|----------------|-------|----------------|-------|-------|----------|------------|------------|-------|----------------|------------|-------|----------------|---------|-------|--------|--------|--------|-------|-------|-------|----------|----------------|-------|-------|----------------|-------|--------------------|-------|
| • | PR<br>R<br>R                                 | žž             | ਲੱ ਤੋ          | ž:      | <del>8</del> <del>8</del> | ž              | ž     | ž ž          | ž                 | ž          | ĕ     | ž:    | ਲੋਂ ਲੋ     | ž     | ž ž            | ×     | ž              | ž.    | ×××            | ž :   | ž ž   | ž ;      | ğ ğ        | ਲੇਲੇ       | ×     | ž ž            | Z Z        | ž     | מ מ            | אָל אָל | מ א   | ž ž    | מ מ    | × ×    | ਲੇਲ   | ž     | א א   | <b>7</b> | × ×            | R :   | S S   | ž ž            | ž     | × ×                | R     |
|   | 23-JI<br>23-JI<br>26-JI<br>27-JI             |                |                |         |                           |                |       |              |                   | 19-JI      | 19-3  | 19-JI | 16-3       |       |                |       |                |       |                |       |       |          |            |            |       |                |            |       |                |         |       |        |        |        |       |       |       |          |                |       |       |                | 0     | 19-м<br>м-81       | 4     |
| • | 3-JUL-19<br>3-JUL-19<br>6-JUL-19<br>7-JUL-19 |                |                |         |                           |                |       |              |                   |            |       |       |            |       |                |       |                |       |                |       |       |          |            |            |       |                |            |       |                |         |       |        |        |        |       |       |       |          |                |       |       |                | ٺ.    |                    | Ċ.    |
|   | 9999   |                |                |         |                           |                |       |              |                   |            |       |       |            |       |                |       |                |       |                |       |       |          |            |            |       |                |            |       |                |         |       |        |        |        |       |       |       |          |                |       |       |                |       |                    |       |
|   | 5066<br>5066<br>5066<br>5066                 | 991            | 991            | 999     | 991                       | 991            | 991   | 991          | 99                | 991        | 99    | 99    | 9 9        | 99    | 9 9            | 991   | 99             | 99    | 99             | 99    | 999   | 99       | 99         | 99         | 99    | 99             | 99         | 999   | 99             | 999     | 9 9   | 99     | 99     | 99     | 9 9   | 99    | 999   | 99       | 99             | 99    | 99    | 99             | 99    | 99                 | 99    |
|   | US-0145<br>US-0145<br>US-0145                | US-01          | 0S-01          | us-01   | US-03                     | 0S-0.          | us-0  | 05-0         | 0-50              | US-0:      | 0-50  | US-0. |            | us-o  | 0S-0           | 0-S   | US-0.          | US-0: | us-0:          | US-0: | US-0  | US-0.    | US-0       | US-0       | us-o  | us-0:          | 0.5-0.     | us-o  | us-0:          | US-0:   | us-o  | US-0:  | US-0   | us-o   | 0S-0  | us-o  | 05-0  | us-o     | US-0           | 0-SD  | US-0  | 08-0           | us-o  | us-0:              | us-0: |
|   | 145218<br>145224<br>145276<br>145913         | 14519          | 14508          | 14508   | 14508                     | 14488<br>14481 | 14463 | 14435        | 14433             | 14433      | 14433 | 14432 | 14408      | 14400 | L4354<br>L4362 | 14297 | 14280<br>14292 | 14239 | 14215          | 14184 | 14099 | 14082    | 14035      | 14035      | 13981 | 13975<br>13976 | 13946      | 13946 | 13945<br>13946 | 13945   | 13945 | 13945  | 13949  | 13945  | 13911 | 13854 | 13809 | 13750    | 1372;<br>1375; | 13678 | 13602 | 13562          | 1351  | 13476<br>13494     | 13437 |
|   | ω 4 το ω                                     | ຫ ຄັ           | 9 ?            | i (i) i |                           | 4 4            | 2     | N 0          | ñ 🍒               | ω.         | ;     | Ŭ.    | 5. č       |       | 4 6            | 7     | ö ü            | Õ     | J &            | 2     | 7 1   | ιώ i     | л <u>4</u> | ω .        | 7.    | ŭ ö            | ω.         | Ϋ́    | 0 9            |         | 9.6   | 4. 17. | 2 .    |        |       |       | 4 .   | 2        | 8 .            |       | 3 12  |                | 4.    | 1 8                | 0     |
|   |  |                |                |         |                           |                |       |              |                   |            |       |       |            |       |                |       |                |       |                |       |       |          |            |            |       |                |            |       |                |         |       |        |        |        |       |       |       |          |                |       |       |                |       |                    |       |
|   |  |                |                |         |                           |                |       |              |                   |            |       |       |            |       |                |       |                |       |                |       |       |          |            |            |       |                |            |       |                |         |       |        |        |        |       |       |       |          |                |       |       |                |       |                    |       |
|   |  |                |                |         |                           |                |       |              |                   |            |       |       |            |       |                |       |                |       |                |       |       |          |            |            |       |                |            |       |                |         |       |        |        |        |       |       |       |          |                |       |       |                |       |                    |       |
|   |  |                |                |         |                           |                |       |              |                   |            |       |       |            |       |                |       |                |       |                |       |       |          |            |            |       |                |            |       |                |         |       |        |        |        |       |       |       |          |                |       |       |                |       |                    |       |
|   |  |                |                |         |                           |                |       |              |                   |            |       |       |            |       |                |       |                |       |                |       |       |          |            |            |       |                |            |       |                |         |       |        |        |        |       |       |       |          |                |       |       |                |       |                    |       |
|   |  |                |                |         |                           |                |       |              |                   |            |       |       |            |       |                |       |                |       |                |       |       |          |            |            |       |                |            |       |                |         |       |        |        |        |       |       |       |          |                |       |       |                |       |                    |       |
|   |  |                |                |         |                           |                |       |              |                   |            |       |       |            |       |                |       |                |       |                |       |       |          |            |            |       |                |            |       |                |         |       |        |        |        |       |       |       |          |                |       |       |                |       |                    |       |
|   |  |                |                |         |                           |                |       |              |                   |            |       |       |            |       |                |       |                |       |                |       |       |          |            |            |       |                |            |       |                |         |       |        |        |        |       |       |       |          |                |       |       |                |       |                    |       |
|   |  |                |                |         |                           |                |       |              |                   |            |       |       |            |       |                |       |                |       |                |       |       |          |            |            |       |                |            |       |                |         |       |        |        |        |       |       |       |          |                |       |       |                |       |                    |       |
|   |  |                |                |         |                           |                |       |              |                   |            |       |       |            |       |                |       |                |       |                |       |       |          |            |            |       |                |            |       |                |         |       |        |        |        |       |       |       |          |                |       |       |                |       |                    |       |
|   |  |                |                |         |                           |                |       |              |                   |            |       |       |            |       |                |       |                |       |                |       |       |          |            |            |       |                |            |       |                |         |       |        |        |        |       |       |       |          |                |       |       |                |       |                    |       |
|   |  |                |                |         |                           |                |       |              |                   |            |       |       |            |       |                |       |                |       |                |       |       |          |            |            |       |                |            |       |                |         |       |        |        |        |       |       |       |          |                |       |       |                |       |                    |       |
|   |  |                |                |         |                           |                | _     |              |                   |            |       |       |            |       |                |       |                |       |                |       |       |          |            |            |       |                |            |       |                |         |       |        |        |        |       |       |       |          |                |       |       | _              |       |                    |       |
|   | PR PR PR                                     | סי סי          | טי טי          | יי טי   | יטינ                      | ט ס            | ٠ م   | סי סי        | סי נ              | יטי        | סי כ  | ייטי  | טי ט       | י קי  | טי ט           | Đ,    | טי ט           | י סי  | סי ס           | י סי  | סיים  | י סי     | טינ        | טי טי      | יטי   | טי ט           | י ש        | ייטיו | סי ט           | ים ים   | יטיו  | סי ס   | ים יכי | י סיו  | סי סי | יטיי  | ים סי | יסי      | סי ס           | י טי  | יסי כ | סי סי          | יטי   | יטיט               | טי    |
|   |  |                |                |         |                           |                | 20 ;  | <b>20</b> 20 | , ×               | <b>≈</b> × |       |       |            |       |                |       |                |       |                |       |       |          |            |            |       |                |            |       |                |         |       |        |        |        |       |       |       |          |                |       |       |                |       |                    |       |
|   | 22-OCT-<br>22-OCT-<br>25-OCT-<br>25-OCT-     | ~ ~            |                |         |                           | mA             | 14-00 | 14-00<br>00  | - 1<br>  2<br>  2 | 20-00      | 25-0  |       | n - 1      | ~ 1   |                | 10 1  | ~ ~            |       | 20-SE          | ~ .   |       |          |            |            |       | 7-             | 26-AU      | ١ψι   | ۰ ۰            | 20-AU   | φ,    | 10     | ωμ     | Ņ      | - 0   | φι    | 06-AU | بأمار    | 05 - AU        | 2.4   | Ψ     | 02-AU<br>02-AU | יאי   | 27 - JU<br>28 - JU | 7-    |
|   | 15015  | 55             | 15             |         |                           | 75             |       | 21           | :::               | 55         | :::   | 12.1  | - :-       | 5:    |                | = :   | 715            | 13:   | 7.5            | 12 1  | - 15  | <u> </u> | :::        | 7.7        | 12.1  | G-19           | G-19       | - L   | . i            | G-19    | G-13  | G-13   | 6-11   | 6-1    | ត-1:  | 6-1   | G-1:  | . i.     | - <u>- 1</u>   | G-15  | 9-1-1 | G-15           | G-1:  | E-11               | L-1   |
|   | 9999   | 99;            | 99;            | 99;     | 99                        | 99             | 99    | 9 9          | 99;               | 99         | 99    | 99;   | 99.        | 99;   | 99,            | 99;   | 99,            | 99;   | 99;            | 99;   | 99;   | 99;      | 99:        | 99;        | 99;   | 99;            | 99.        | 99;   | 99;            | 99;     | 99;   | 99;    | 99;    | ; 66   | 99:   | 99;   | 99.   | 999      | 99;            | 99;   | 99;   | 99;            | 99;   | 99,                | ; 66  |
|   | SD66<br>SD66<br>SD66<br>SD66                 | 990            | 991            | 991     | 991                       | 166<br>166     | 991   | 999          | 99                | 991        | 991   | 166   | 991        | 991   | 991            | 991   | 166<br>166     | 991   | 991            | 991   | 991   | 991      | 991        | 991        | 991   | 991            | 991        | 991   | 991            | 991     | 99    | 99     | 991    | 99     | 999   | 99    | 991   | 999      | 99             | 991   | 99    | 999            | 99    | 999                | 991   |
|   | 78-010<br>78-010<br>78-010                   | ავ-01<br>ავ-01 | 7S-01<br>7S-01 | JS-01   | JS-01                     | JS-01<br>JS-01 | JS-01 | JS-01        | JS-01             | JS-01      | JS-01 | JS-01 | JS-01      | JS-01 | 75-01<br>10-8  | JS-01 | 75-01<br>0-01  | JS-01 | 75-01<br>10-81 | JS-01 | US-01 | 7S-01    | US-01      | US-01      | US-01 | US-01          | US-01      | US-01 | US-01          | US-01   | US-01 | US-01  | US-01  | US-01  | US-01 | US-01 | US-01 | US-01    | US-01          | US-01 | US-01 | US-01          | US-01 | US-01              | US-01 |
|   | 60981<br>60989<br>61404<br>61405             |                |                |         |                           |                |       |              |                   |            |       |       |            |       |                |       |                |       |                |       |       |          |            |            |       |                |            |       |                |         |       |        |        |        |       |       |       |          |                |       |       |                |       |                    |       |
|   | 5491   | 0.5            | . 4            |         | 1 <u>:</u> :              | - 00           | 7.    |              |                   | · ·        | - ω   |       | <u>ن</u> د | 5 .   | ۰,             |       |                | o (   | o .o           | 9 0   |       | 0 .      | .0         | <b>σ</b> ο |       | י נים          | <b>.</b> . | 0.    | <u>ه</u> د     | ω κ     |       | л α ο  |        | ٠ بـ : | 9 -   |       | ω σ   | · ω̄ ;   | ว กั           |       | . 60  | φ.             | 0     | - 0                | œ     |
|   |  |                |                |         |                           |                |       |              |                   |            |       |       |            |       |                |       |                |       |                |       |       |          |            |            |       |                |            |       |                |         |       |        |        |        |       |       |       |          |                |       |       |                |       |                    |       |
|   |  |                |                |         |                           |                |       |              |                   |            |       |       |            |       |                |       |                |       |                |       |       |          |            |            |       |                |            |       |                |         |       |        |        |        |       |       |       |          |                |       |       |                |       |                    |       |

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   25-FEB-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mays subsp. mays.
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l Similarity 100.0%;
22; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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O; Mismatches
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1.8e-15;
hes 0;
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   27-MAY-1999
21-MAY-1999
01-JUN-1999
07-JUN-1999
110-JUN-1999
110-JUN-1
9908-0137528
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9908-0137528
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9908-0138604
9908-0139453
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9908-0142300
9908-0144331
9908-0145086
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9908-0145287
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9908-0145283
9908-0145283
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DB 21; 1.8e-15; 0

Length Indels 83

0

Gaps

0

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04-AUG-1999
06-AUG-1999
05-AUG-1999
06-AUG-1999
06-AUG-1999
06-AUG-1999
11-AUG-1999
11-AUG-1999
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29-AUG-1999
21-AUG-1999
21-AUG
             99US-0147204

99US-0147204

99US-0147302

99US-0147192

99US-0147303

99US-0148171

99US-0148311

99US-0148341

99US-0148341

99US-0148341

99US-0149368

99US-0149175

99US-0149175

99US-0149426

99US-0149175

99US-0149175

99US-0149175

99US-0149175

99US-0149175

99US-0151066

99US-0151060

99US-0160767

99US-0160770

99US-0160770

99US-016100

99US-016100
     RESULT 38
AAG3287
XX AAG32
XX Prote KW Prote KW Prote KW Prote Can max AAG32
XX Explosion Color of Canada AAG32
XX Explosion Ca
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  25-FEB-1999

05-MAR-1999

09-MAR-1999

23-MAR-1999

25-MAR-1999

29-MAR-1999

16-APR-1999

16-APR-1999

16-APR-1999

23-APR-1999

23-APR-1999

23-APR-1999

23-APR-1999

24-APR-1999

26-APR-1999

30-APR-1999

30-APR-1999

30-APR-1999

30-APR-1999

14-MAY-1999

15-MAY-1999

16-MAY-1999

17-MAY-1999

18-MAY-1999

19-MAY-1999

21-MAY-1999

21-MA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard;
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99US-0121825
99US-0123180)
99US-0125788
99US-0126786
99US-0126786
99US-0128234
99US-0128234
99US-0130610
99US-0130610
99US-0130610
99US-0130449
99US-0131449
99US-0132486
99US-0132486
99US-0132486
99US-0132487
99US-0134276
99US-0137522
99US-0137528
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Pred. No.
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39760.

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110-JUN-1999
114-JUN 1999
116-JUN 1999
116-JUN 1999
117-JUN 1999
118-JUN 1999
118-J
 99US-0138540
99US-0139157
99US-0139453
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99US-01491842
99US-0144085
99US-0144085
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99US-0144331
99US-0144333
99US-01445184
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27-AUG-1999
28-SEP-1999
29-CCT-1999
21-CCT-1999
21-CCT-1999
21-CCT-1999
21-CCT-1999
22-CCT-1999
1 KVHGSLARAGKVRGQTPKVAKQ
                        th 37.3%; Score 22; DB 21; Similarity 100.0%; Pred. No. 1.9e-1 22; Conservative 0; Mismatches
                                                                           9908-0147935.
9908-0148119.
9908-0148119.
9908-014826.
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9908-0151065.
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22
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                                                Length 84;
                          Indels
                          0;
                          Gaps
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| PR PR R PR R PR R PR R P | ט מי  |   | Db  RESU AAGG XXX XXX XXX XXX XXX XXX XXX XXX XX   |          |
|---|---|---|--|----------|
| JUN-15<br>JUN-15<br>JUN-15<br>JUN-19<br>JUN-19<br>JUN-19  | MAY-19<br>MAY-19<br>MAY-19<br>MAY-19<br>MAY-19<br>MAY-19<br>MAY-19<br>MAY-19<br>JUN-19<br>JUN-19  | 09-MAR-1999<br>23-MAR-1999<br>25-MAR-1999<br>29-MAR-1999<br>01-APR-1999<br>08-APR-1999<br>16-APR-1999<br>16-APR-1999<br>21-APR-1999<br>21-APR-1999<br>23-APR-1999<br>23-APR-1999<br>23-APR-1999<br>23-APR-1999<br>04-MAY-1999<br>06-MAY-1999<br>06-MAY-1999 | X  |          |
| 00000000  |   | 99US-0125488<br>99US-0125788<br>99US-01264<br>99US-0126785<br>99US-0127462<br>99US-0128714<br>99US-0129845<br>99US-0130449<br>99US-0130449<br>99US-0130449<br>99US-0130489<br>99US-0132486<br>99US-0132485<br>99US-0132486                                  | GKYRGQTP   |          |
| ייטיטיטיטיטיטייי<br>דעטיטיטיטיטיטיטיטיטיטיטיטיטיטיטיטיטיטיטי  | 2   |   |  | - PI     |
| 09-AUG-11<br>09-AUG-12<br>10-AUG-13<br>11-AUG-11<br>12-AUG-11<br>13-AUG-11<br>13-AUG-11<br>16-AUG-11  | 23-JUL-11<br>26-JUL-11<br>27-JUL-11<br>27-JUL-11<br>27-JUL-11<br>27-JUL-11<br>27-JUL-11<br>28-JUL-11<br>28-JUL-11<br>02-AUG-11<br>03-AUG-11<br>04-AUG-11<br>05-AUG-11<br>05-AUG-11<br>06-AUG-11 | 15-301-11-11-11-11-11-11-11-11-11-11-11-11-1  | 18-JUN-11 18-JUN | 18-JUN-1 |
| 9908-011<br>9908-011<br>9908-011<br>9908-011<br>9908-011<br>9908-011  | 99US-0145218<br>99US-0145224<br>99US-0145213<br>99US-0145913<br>99US-0145951<br>99US-0146386<br>99US-0146386<br>99US-0147038<br>99US-0147038<br>99US-0147303<br>99US-0147303                    | 9908-011<br>9908-011<br>9908-011<br>9908-011<br>9908-011<br>9908-011<br>9908-011<br>9908-011<br>9908-011  | 999) 99US-0139456<br>999) 99US-0139459<br>999S-0139459<br>999S-0139460<br>999S-0139463<br>999S-0139463<br>999S-0139463<br>999S-013989<br>99US-0139817<br>999S-0140353<br>999) 99US-0140354<br>999S-0140353<br>999) 99US-0140823<br>999) 99US-0141287<br>990S-014287<br>990S-014287<br>990S-014287<br>990S-0142823<br>999) 99US-0142823<br>999) 99US-0142823<br>999) 99US-0142823<br>999-99US-0142823<br>999-99US-0142823<br>999-99US-0142823<br>999-99US-0142823<br>999-99US-0142823<br>999-99US-0142823<br>999-99US-0142823<br>999-99US-0142823<br>999-99US-0142823<br>999-99US-0142823   | 99US-01  |

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Query Match
Best Local S
Matches 23
                                                                                                                                    17-AUG-1999
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20-AUG-1999
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21-AUG-1999
23-AUG-1999
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27-AUG-1999
27-AUG-1999
31-AUG-1999
31-SEP-1999
32-SEP-1999
32-SEP-1999
32-SEP-1999
33-SEP-1999
34-OCT-1999
35-OCT-1999
36-OCT-1999
31-OCT-1999
31-OCT-1999
31-OCT-1999
32-OCT-1999
   AAG32886 standard; Protein; 110 AA.
                                                     KVHGSLARAGKVRGQTPKVAKQ
                                                                                            ch 37.3%;
l Similarity 100.0%
22; Conservative
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99US-0151086
99US-0151080
99US-0151438
99US-0151375
99US-0151403
99US-0151403
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99US-0155486
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99US-0155859
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99US-0159331
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99US-0149426.
99US-0149722.
99US-0149723.
                                                                                         J.0%;
0;
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                                                                        22
                                                                                            Score 22; DB 21;
Pred. No. 2e-15;
0; Mismatches
                                                                                              0
                                                                                                            Length 93;
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                                                                                             0;
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25-FEB-1999
05-MAR-1999
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21-APR-1999
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26-MAY-1999
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11-JUN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-SEP-2000
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 9905-0123180
9905-0125788
9905-0125788
9905-012664
9905-0126264
9905-0128734
9905-0128734
9905-0130077
9905-0130499
9905-0130499
9905-0132486
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9905-0134218
9905-0134218
9905-013421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NO:
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RESULT 40 AAG32886 ID AAG32

Qy 밁

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RESULT 41
AAG26728 :
ID AAG26728 :
XX
AC AAG26728;
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DT 17-OCT-200
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31-AUG-1999
31-SEP-1999
31-SEP-1999
32-SEP-1999
32-SEP-1999
23-SEP-1999
24-SEP-1999
25-OCT-1999
36-OCT-1999
37-OCT-1999
38-OCT-1999
38-OCT-1999
39-OCT-1999
                   Zea mays protein fragment SEQ
                                                         17-OCT-2000
                                                                                                                                                                                                                              51
                                                                                                                                                                                                                                                                                                 / Match 37.3%;
Local Similarity 100.0%
nes 22; Conservative
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| 99US - 0127462. 99US - 0128714. 99US - 013047. 99US - 0130449. 99US - 0131449. 99US - 013248. 99US - 0134218. 99US - 0134219.   | n; signal transduction pathway; genetic mapping; gene expressio corn.  301439.  121825. 12188. 125788. 126785.   |
| אק ק<br>אק ק<br>אק ק<br>אק ק<br>אק ק<br>אק ק<br>אק ק<br>אק ק   | metabolic pathway;  promoter;  pr |
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07-SEP-1999;
10-SEP-1999;
         Tax interacting protein clone 2; TIP-2; GIPC; antigen; tumour; breast cancer; prostate cancer; monoclonal antibody; 27.B1; 27.F7; thyroid cancer; tetanus toxin; infection; HIT; hanta virus; Ebola; human immunodeficiency virus infection; enzyme dysfunction; hormone dysfunction; autoimmune disease; lupus; rheumatoid arthritis; immune dysfunction; septicaemia; human.
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13-SEP-1
15-SEP-1
                                                                                                                                          ABG34133 standard; Protein; 230
                                                                             Human seb4B protein.
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99US-0160741.
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ABG34132;

ABG34132 standard; Protein; 459

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34 RRMQYNRRFVNVVPTFGKKKG

21 54 Similarity 100 21; Conservative

Score 21; DB 23; Pred. No. 5.1e-140; Mismatches (

.1e-14;

Length 230;

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Gaps

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cancer cells, in a subject. A composition comprising the mab is useful for treating or preventing a condition in a subject who previously exhibited the condition, where the condition is associated with cancer (thyroid, breast or prostate cancer), tumour (benign), toxin (tetanus, as Hanta virus, influence or spider venom), infectious agent (such as Hanta virus, influence). The prostate cancer or spider venom, infectious agent (such cas Hanta virus, influence). Ebola, human papilloma virus, influence, Ebola, human papilloma virus, or Ciryptococcus, Streptococcus, Klebsiella, Escherichia coli, anthrax or Ciryptococcus, enzyme dysfunction (hyperactivity or overproduction of the hormone), autoimmune disease (lupus, thyroiditis, graft versus host chormone), autoimmune disease (lupus, thyroiditis, graft versus host disease, transplantation rejection or rheumatoid arthritis), immune dysfunction (CD) or CD4 mediated), viral antigen, bacterial antigen, rejection of a transplanted tissue, or the condition is septicaemia, sepsis, septic shock, viraemia, bacteraemia, fungaemia. The present sequence is an additional human cancer associated marker which are be used in the production of monor or the condition of the present sequence is an additional human cancer associated marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                binds and forms a complex with TIP-2 (Tax interacting protein clone 2, also known as GIPC) antigen located on the surface of human cancer cells, where mab binds to the same antigen as monoclonal antibody 27.Bl or 27.F7 produced by hybridoma 27.Bl or 27.F7 of ATCC Designation No. PTA-1599 or 1598, respectively. The mab is useful for detecting TIP-2 antigen bearing cancer cells, for diagnosing cancer in a subject by detecting TIP-2 antigen-bearing cancer cells, for in vivo diagnosis of cancer in a subject, for delivering exogenous material to TIP-2 antigen-bearing cancer cells of a human subject, for inducing apoptosis of TIP-2 antigen bearing cancer in a human subject, for inducing apoptosis of TIP-2 antigen bearing cells, for detecting the presence of TIP-2 antigen bearing cancer cells, for detecting the progression of cancer, where the cancer cells are TIP-2 antigen-bearing the progression of cancer, where the cancer cells are TIP-2 antigen-bearing the progression of cancer, where the cancer cells are TIP-2 antigen-bearing the progression of cancer, where the cancer cells are TIP-2 antigen-bearing the progression of cancer, where the cancer cells are TIP-2 antigen-bearing the progression of cancer, where the cancer cells are TIP-2 antigen-bearing cancer cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New monoclonal antibody which specifically binds and forms complex with TIP-2 antigen located on surface of human cancer cells, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-362353/39
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                                                                                                                                                                         can be used in the production of monoclonal antibodies.
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                                                                                                                          230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41B; 276pp; English.
35.6%; 5-
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promoter;

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The invention relates to a monoclonal (mAb) antibody which specifically calso known as GIPC) antigen located on the surface of human cancer cells, where mAb binds to the same antigen as monoclonal antibody 27.B1 cancer mAb binds to the same antigen as monoclonal antibody 27.B1 cancer cells, respectively. The mAb is useful for detecting TIP-2 antigen-bearing cancer cells, for diagnosing cancer in a subject by detecting TIP-2 antigen-bearing cancer cells, for in vivo diagnosis of cancer in a subject, for detecting the pearing cancer cells, for in vivo diagnosis of cancer in a subject, for inducing apoptosis of TIP-2 antigen bearing cancer in a subject by the pragnature of TIP-2 antigen bearing cancer in a human subject. for treating cancer in a human cells, for immunohistochemical screening of a tissue section from a tumour sample for the presence of TIP-2 antigen bearing cancer calls, for immunohistochemical screening of a tissue section from a tumour sample cancer cells, in a subject. A composition comprising the mAb is useful cancer cells, in a subject who previously canthrax, botulinum, snake venom or spider venom), infectious agent (such as Hanta virus, transplantation, (hyperactivity or overproduction of the cancer, transplantation rejection or rebunated arthritis), immune cells are the condition of the hormone), autoimmune disease (lupus, thyroiditis, graft versus host condition (Day antigen, reflection or rebunated tissue, or the condition condition or reflection or repeated tissue, or the condition cancer cancer in a subject who previously immune condition is a saccial antigen, reflection or rebunated tissue, or the condition cancer cancer in a subject who previously immune cancer cancer in a subject who previously immune cancer cancer in a subject who previously immune cancer cancer in a subject i
                                                             Query Match
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                                                                                                                                                                                                                         eukaryotic antigen, rejection of a transplanted tissue, or the condition is septicaemia, sepsis, septic shock, viraemia, bacteraemia, fungaemia. The present sequence is an additional human cancer associated marker
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                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diagnosing and treating cancer in a human subject
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100.0%;
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                                                       Score 21; DB 23; Pred. No. 9.3e-1
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                                   Mismatches
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                                                       9.3e-14;
                                                                                     Length 459;
                                Indels
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RESULT 44
AAG20231
ID AAG30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         termination sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana protein fragment SEQ ID
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990S-01347370.
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990S-0134941.
990S-0135124.
990S-013523.
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99US-0130077.
99US-0130449.
99US-0139119.
99US-0139452.
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99US-0127462
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99US-0137502.
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99US-0136392.
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RESULT 45
AAU31057
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Matches 20
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Pred. No. 1.9
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18-JUN 1999
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99US-0139454 99US-0139457 99US-0139460 99US-0139463 99US-0139463 99US-0139463 99US-0139463 99US-0139463 99US-014063 99US-014063 99US-014063 99US-014063 99US-014063 99US-014186 99US-014186

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Search completed: February 6, 2003, 21:30:53 Job time: 37 secs
                                                                    В
                                                                                                οy
                                                                                                                                                                                                                             The invention relates to novel human secreted polypeptides. The CC polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and in the corresponding the polyferation; to regulate haematopoiesis; and in the cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and concerned to expression and/or stimulation; as anti-inflammatory agents; and concerned to expression and/or stimulation; of the invention.
                                                                                                                                  Query Match 32.3
Best Local Similarity 100
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 20; Page 397; 765pp; English.
                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-611725/70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HYSE-) HYSEQ INC.
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26-JAN-2001; 2001US-0770160.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; vaccination; gene therapy; nutritional supplement; stem cell proliferation; haematopoiesis; nerve tissue regeneration; immune suppression; immune stimulation; anti-inflammatory; leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU31057 standard; Protein; 229 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel human secreted protein #1548.
                                                                 Liu C,
                                                                                                                                                                                                      229 AA;
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                                                                                                                           32.2%; 5cc
100.0%; Pr
                                                                                                                                                 Score 19; DB 22;
; Pred. No. 6.4e-12;
                                                                                                                                   Mismatches
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                                                                                                                                                                 Length 229;
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(Olden) XNV TE 39Vct SIHI